1180211

From:	Hutzell, Paula
Sent:	Monday, March 29, 2004 8:30 AM
To:	Holleran, Anne; STIC-Biotech/ChemLib
Cc:	Chan, Christina
Subject:	RE: RUSH sequence search for 09/477,082

approved

-----Original Message-----
From:	Holleran, Anne
Sent:	Friday, March 26, 2004 12:02 PM
To:	Hutzell, Paula
Cc:	Chan, Christina
Subject:	FW: RUSH sequence search for 09/477,082

-----Original Message-----
From:	Holleran, Anne
Sent:	Friday, March 26, 2004 12:01 PM
To:	Chan, Christina
Subject:	RUSH sequence search for 09/477,082

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following for 09/477,082

interference databases **only** search of SEQ ID NO: 1(na)
interference databases **only** search of SEQ ID NO: 2(na)

commercial and interference database search of SEQ ID NO: 29, 30, 31, 32, 33, 34(na), these are primer sequences *Please perform a Score/Length sequence search for the primer seqeunces (SEQ ID NO: 29-34) with a minimum hit length of 15 and a maximum hit lenght of 40, and a score over length value of 90% or greater*

SEQ ID NO: 1 and SEQ ID NO: 2 are two different regions of the same gene

Anne Holleran
AU: 1642
Tel: (571) 272-0833
RM: Remsen, 3A14

mailbox: Remsen, 3C18

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_____	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_____	Bibliographic:_____	DRLink:_____
Date Completed:__3/31__	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_____
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 12:49:34 ; Search time 2672.94 Seconds				
(without alignments)				
10864.389 Million cell updates/sec				
Title: US-09-477-082-1				
Perfect score: 670				
Sequence: 1 aagcgctccaagacacgatt..........ggggttaaataaagcgcttt 670				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 3470272 seqs, 21671516995 residues				
Total number of hits satisfying chosen parameters: 1364278				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : GenEmbl:*				
1: gb_ba:*				
2: gb_htg:*				
3: gb_in:*				
4: gb_om:*				
5: gb_ov:*				
6: gb_pat:*				
7: gb_ph:*				
8: gb_pl:*				
9: gb_pr:*				
10: gb_ro:*				
11: gb_sts:*				
12: gb_sy:*				
13: gb_un:*				
14: gb_vi:*				
15: em_ba:*				
16: em_fun:*				
17: em_hum:*				
18: em_in:*				
19: em_mu:*				
20: em_om:*				
21: em_or:*				
22: em_ov:*				

23: em_pat:*						
24: em_ph:*						
25: em_pl:*						
26: em_ro:*						
27: em_sts:*						
28: em_un:*						
29: em_vi:*						
30: em_htg_hum:*						
31: em_htg_inv:*						
32: em_htg_other:*						
33: em_htg_mus:*						
34: em_htg_pln:*						
35: em_htg_rod:*						
36: em_htg_mam:*						
37: em_htg_vrt:*						
38: em_sy:*						
39: em_htgo_hum:*						
40: em_htgo_mus:*						
41: em_htgo_other:*						

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	S/L
5313	13.4	2	15	6	AR208417	0.893333
c5314	13.4	2	15	6	AX802132	0.893333
5315	13.4	2	15	6	BD208917	0.893333
8164	13	1.9	15	6	AX009449	0.866667
c1846	14.4	2.1	17	6	AX758412	0.847059
1847	14.4	2.1	17	8	ATH526809	0.847059
1848	14.4	2.1	17	8	ATH526810	0.847059
5316	13.4	2	16	6	AR080878	0.8375
c5317	13.4	2	16	6	BD266396	0.8375
c5318	13.4	2	16	6	BD104574	0.8375
1082	15	2.2	18	6	AX378655	0.833333
15795	12.4	1.9	15	6	A52100	0.826667
15796	12.4	1.9	15	6	A52101	0.826667
15797	12.4	1.9	15	6	A52128	0.826667
15798	12.4	1.9	15	6	A52129	0.826667
15799	12.4	1.9	15	6	A65237	0.826667
15800	12.4	1.9	15	6	A66708	0.826667
15801	12.4	1.9	15	6	A66711	0.826667
15802	12.4	1.9	15	6	A68206	0.826667
15803	12.4	1.9	15	6	A68260	0.826667

← No hits Score/Length 90% or above

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 11:54:58 ; Search time 289.564 Seconds				
(without alignments)				
9829.571 Million cell updates/sec				
Title: US-09-477-082-1				
Perfect score: 670				
Sequence: 1 aagcgctccaagacacgatt.........ggggttaaataaagcgcttt 670				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 3373863 seqs, 2124099041 residues				
Total number of hits satisfying chosen parameters: 2072792				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : N_Geneseq_29Jan04:*				
1: geneseqn1980s:*				
2: geneseqn1990s:*				
3: geneseqn2000s:*				
4: geneseqn2001as:*				
5: geneseqn2001bs:*				
6: geneseqn2002s:*				
7: geneseqn2003as:*				
8: geneseqn2003bs:*				
9: geneseqn2003cs:*				
10: geneseqn2004s:*				
Pred. No. is the number of results predicted by chance to have a				
score greater than or equal to the score of the result being printed,				
and is derived by analysis of the total score distribution.				

		SUMMARIES				
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L

3719	14	2.1	15	4	AAH20313	0.933333
3720	14	2.1	15	6	ABK98147	0.933333

7279	13.4	2	15	3	AAZ64339	0.893333
c7280	13.4	2	15	4	AAH74112	0.893333
7281	13.4	2	15	6	AAD39760	0.893333
7282	13.4	2	15	6	ABX01392	0.893333
11340	13	1.9	15	3	AAZ48115	0.866667
c2401	14.4	2.1	17	6	ABN07749	0.847059
c2402	14.4	2.1	17	6	ABN07750	0.847059
c2403	14.4	2.1	17	9	ADB41410	0.847059
c17300	12.6	1.9	15	6	ABA03942	0.84
c7283	13.4	2	16	6	ABL31189	0.8375
1374	15	2.2	18	6	ABK41196	0.833333
21562	12.4	1.9	15	2	AAQ29530	0.826667
21563	12.4	1.9	15	2	AAQ81114	0.826667
21564	12.4	1.9	15	2	AAT55623	0.826667
21565	12.4	1.9	15	2	AAT31819	0.826667
c21566	12.4	1.9	15	2	AAX64708	0.826667
21567	12.4	1.9	15	2	AAT37116	0.826667
c21568	12.4	1.9	15	2	AAT50251	0.826667
21569	12.4	1.9	15	2	AAV07762	0.826667
21570	12.4	1.9	15	2	AAV07759	0.826667
21571	12.4	1.9	15	2	AAV06230	0.826667
21572	12.4	1.9	15	2	AAX33998	0.826667
21573	12.4	1.9	15	2	AAV06801	0.826667
21574	12.4	1.9	15	2	AAV48551	0.826667
21575	12.4	1.9	15	2	AAV06817	0.826667
21576	12.4	1.9	15	3	AAZ64338	0.826667
21577	12.4	1.9	15	3	AAA07813	0.826667
21578	12.4	1.9	15	4	AAH20310	0.826667
21579	12.4	1.9	15	4	AAF31459	0.826667
21580	12.4	1.9	15	4	AAF59902	0.826667
21581	12.4	1.9	15	4	AAF59905	0.826667
21582	12.4	1.9	15	4	AAF31566	0.826667
21583	12.4	1.9	15	4	AAF52237	0.826667
c21584	12.4	1.9	15	4	AAF52606	0.826667
21585	12.4	1.9	15	4	AAF52236	0.826667
c21586	12.4	1.9	15	4	AAF52607	0.826667
21587	12.4	1.9	15	4	AAH28548	0.826667
21588	12.4	1.9	15	4	AAF97971	0.826667
c21589	12.4	1.9	15	6	AAD41857	0.826667
21590	12.4	1.9	15	6	ABX01391	0.826667
21591	12.4	1.9	15	6	ABK98173	0.826667
21592	12.4	1.9	15	6	ABK98172	0.826667
21593	12.4	1.9	15	6	ABK98144	0.826667
21594	12.4	1.9	15	7	ABX16342	0.826667
21595	12.4	1.9	15	9	ADC66181	0.826667
21596	12.4	1.9	15	9	ADC66180	0.826667
c3721	14	2.1	17	7	ABT40012	0.823529
c3722	14	2.1	17	9	ADE25256	0.823529
1660	14.8	2.2	18	2	AAX03843	0.822222

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OM nucleic - nucleic search, using sw model						
Run on:	March 29, 2004, 16:27:20 ; Search time 66.3879 Seconds					
	(without alignments)					
	5600.675 Million cell updates/sec					
Title:	US-09-477-082-1					
Perfect score: 670						
Sequence:	1 aagcgctccaagacacgatt.........ggggttaaataaagcgcttt 670					
Scoring table: IDENTITY_NUC						
	Gapop 10.0 , Gapext 1.0					
Searched:	682709 seqs, 277475446 residues					
Total number of hits satisfying chosen parameters:		718054				
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
	Maximum Match 100%					
	Listing first 65000 summaries					
Database :	Issued_Patents_NA:*					
	1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*					
	2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*					
	3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*					
	4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*					
	5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*					
	6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*					
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
		SUMMARIES				
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
--						
3076	13.4	2	15	4	US-09-540-824-15	0.893333
c1093	14.4	2.1	17	4	US-09-866-108A-7741	0.847059
c1094	14.4	2.1	17	4	US-09-866-108A-7742	0.847059
3077	13.4	2	16	2	US-08-459-434-6	0.8375
c9064	12.4	1.9	15	1	US-08-142-785-5	0.826667
9065	12.4	1.9	15	1	US-08-142-785-6	0.826667

c9066	12.4	1.9	15	1	US-07-799-824-4	0.826667
c9067	12.4	1.9	15	1	US-07-976-103A-4	0.826667
c9068	12.4	1.9	15	1	US-08-363-240A-665	0.826667
9069	12.4	1.9	15	1	US-08-426-807-1	0.826667
9070	12.4	1.9	15	1	US-08-311-486C-16	0.826667
c9071	12.4	1.9	15	1	US-07-892-902-6	0.826667
9072	12.4	1.9	15	1	US-07-892-902-7	0.826667
c9073	12.4	1.9	15	2	US-08-473-481-4	0.826667
c9074	12.4	1.9	15	2	US-08-585-684B-202	0.826667
9075	12.4	1.9	15	2	US-08-459-434-1	0.826667
c9076	12.4	1.9	15	3	US-09-038-073-202	0.826667
c9077	12.4	1.9	15	3	US-08-338-352-5	0.826667
9078	12.4	1.9	15	4	US-09-202-294-1	0.826667
c9079	12.4	1.9	15	4	US-08-599-738A-4	0.826667
9080	12.4	1.9	15	4	US-09-612-531-4	0.826667
9081	12.4	1.9	15	4	US-09-612-531-8	0.826667
9082	12.4	1.9	15	4	US-09-612-531-9	0.826667
9083	12.4	1.9	15	4	US-09-612-531-10	0.826667
9084	12.4	1.9	15	4	US-09-612-531-14	0.826667
9085	12.4	1.9	15	4	US-09-612-531-15	0.826667
9086	12.4	1.9	15	4	US-09-612-531-16	0.826667
9087	12.4	1.9	15	4	US-09-612-531-17	0.826667
9088	12.4	1.9	15	4	US-09-612-531-18	0.826667
9089	12.4	1.9	15	4	US-09-612-531-19	0.826667
9090	12.4	1.9	15	4	US-09-612-531-20	0.826667
9091	12.4	1.9	15	4	US-09-612-531-21	0.826667
9092	12.4	1.9	15	4	US-09-612-531-22	0.826667
9093	12.4	1.9	15	4	US-09-612-531-23	0.826667
9094	12.4	1.9	15	4	US-09-612-531-24	0.826667
9095	12.4	1.9	15	4	US-09-612-531-25	0.826667
9096	12.4	1.9	15	4	US-09-142-212A-3	0.826667
9097	12.4	1.9	15	4	US-09-142-212A-4	0.826667
9098	12.4	1.9	15	4	US-09-142-212A-5	0.826667
9099	12.4	1.9	15	4	US-09-142-212A-6	0.826667
9100	12.4	1.9	15	4	US-09-142-212A-9	0.826667
9101	12.4	1.9	15	4	US-09-142-212A-13	0.826667
9102	12.4	1.9	15	4	US-09-349-040A-6	0.826667
9103	12.4	1.9	15	4	US-09-349-040A-7	0.826667
9104	12.4	1.9	15	4	US-09-349-040A-8	0.826667
9105	12.4	1.9	15	4	US-09-753-943D-3	0.826667
9106	12.4	1.9	15	4	US-09-753-943D-4	0.826667
9107	12.4	1.9	15	4	US-09-753-943D-6	0.826667
9108	12.4	1.9	15	4	US-09-753-943D-7	0.826667
9109	12.4	1.9	15	4	US-09-753-943D-8	0.826667
9110	12.4	1.9	15	4	US-09-753-943D-9	0.826667
c9111	12.4	1.9	15	4	US-09-753-943D-10	0.826667
c9112	12.4	1.9	15	4	US-09-753-943D-11	0.826667
c9113	12.4	1.9	15	4	US-09-753-943D-12	0.826667
c9114	12.4	1.9	15	4	US-09-753-943D-13	0.826667

GenCore version 5.1.6					
Copyright (c) 1993 - 2004 Compugen Ltd.					
OM nucleic - nucleic search, using sw model					
Run on:	March 29, 2004, 18:10:30 ; Search time 258.96 Seconds				
	(without alignments)				
	9632.441 Million cell updates/sec				
Title:	US-09-477-082-1				
Perfect score: 670					
Sequence:	1 aagcgctccaagacacgatt..........ggggttaaataaagcgcttt 670				
Scoring table: IDENTITY_NUC					
	Gapop 10.0 , Gapext 1.0				
Searched:	2458946 seqs, 1861504846 residues				
Total number of hits satisfying chosen parameters:		1244038			
Minimum DB seq length: 15					
Maximum DB seq length: 40					
Post-processing: Minimum Match 0%					
	Maximum Match 100%				
	Listing first 65000 summaries				
Database :	Published_Applications_NA:*				
	1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*				
	2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*				
	3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*				
	4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*				
	5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*				
	6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*				
	7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*				
	8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*				
	9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*				
	10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*				
	11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*				
	12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*				
	13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*				
	14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*				
	15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*				
	16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*				
	17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*				
	18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*				
Pred. No. is the number of results predicted by chance to have a					
score greater than or equal to the score of the result being printed,					
and is derived by analysis of the total score distribution.					

Result No.	Score	% Query Match	Length	DB	ID	S/L
		SUMMARIES				
4092	13.4	2	15	9	US-09-504-231A-1174	0.893333
4093	13.4	2	15	9	US-09-274-553D-1174	0.893333
c1318	14.4	2.1	17	9	US-09-866-108-7741	0.847059
c1319	14.4	2.1	17	9	US-09-866-108-7742	0.847059
1320	14.4	2.1	17	10	US-09-730-289B-27	0.847059
c1321	14.4	2.1	17	14	US-10-230-006-50	0.847059
c1322	14.4	2.1	17	14	US-10-230-006-547	0.847059
1323	14.4	2.1	17	15	US-10-300-683-252	0.847059
c4094	13.4	2	16	15	US-10-297-068-678	0.8375
690	15	2.2	18	12	US-10-333-429-444	0.833333
12708	12.4	1.9	15	9	US-09-504-231A-1173	0.826667
12709	12.4	1.9	15	9	US-09-274-553D-1173	0.826667
12710	12.4	1.9	15	14	US-10-247-893-4	0.826667
12711	12.4	1.9	15	14	US-10-247-893-8	0.826667
12712	12.4	1.9	15	14	US-10-247-893-9	0.826667
12713	12.4	1.9	15	14	US-10-247-893-10	0.826667
12714	12.4	1.9	15	14	US-10-247-893-14	0.826667
12715	12.4	1.9	15	14	US-10-247-893-15	0.826667
12716	12.4	1.9	15	14	US-10-247-893-16	0.826667
12717	12.4	1.9	15	14	US-10-247-893-17	0.826667
12718	12.4	1.9	15	14	US-10-247-893-18	0.826667
12719	12.4	1.9	15	14	US-10-247-893-19	0.826667
12720	12.4	1.9	15	14	US-10-247-893-20	0.826667
12721	12.4	1.9	15	14	US-10-247-893-21	0.826667
12722	12.4	1.9	15	14	US-10-247-893-22	0.826667
12723	12.4	1.9	15	14	US-10-247-893-23	0.826667
12724	12.4	1.9	15	14	US-10-247-893-24	0.826667
12725	12.4	1.9	15	14	US-10-247-893-25	0.826667
c12726	12.4	1.9	15	14	US-10-024-818-4	0.826667
c12727	12.4	1.9	15	14	US-10-294-203-4	0.826667
c12728	12.4	1.9	15	15	US-10-440-850-111	0.826667
12729	12.4	1.9	15	15	US-10-444-347-28	0.826667
c2046	14	2.1	17	14	US-10-338-777-231	0.823529
c6553	13	1.9	16	15	US-10-297-068-870	0.8125
c2511	13.8	2.1	17	9	US-09-866-108-7743	0.811765
c2512	13.8	2.1	17	9	US-09-866-108-7744	0.811765
c2513	13.8	2.1	17	9	US-09-866-108-9786	0.811765
2514	13.8	2.1	17	9	US-09-866-108-10318	0.811765
2515	13.8	2.1	17	9	US-09-263-959-10	0.811765
2516	13.8	2.1	17	9	US-09-263-959-13	0.811765
c2517	13.8	2.1	17	10	US-09-780-533A-2024	0.811765
c2518	13.8	2.1	17	10	US-09-740-332-1246	0.811765
c2519	13.8	2.1	17	10	US-09-817-879-1246	0.811765

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on:	March 29, 2004, 16:32:15 ; Search time 2575.47 Seconds			
	(without alignments)			
	9153.537 Million cell updates/sec			
Title:	US-09-477-082-1			
Perfect score: 670				
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Scoring table: IDENTITY_NUC				
	Gapop 10.0 , Gapext 1.0			
Searched:	37577330 seqs, 17593059518 residues			
Total number of hits satisfying chosen parameters:	26876998			
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
	Maximum Match 100%			
	Listing first 65000 summaries			
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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16424	14.4	2.1	16	21	US-09-528-209A-1600	0.9
c16425	14.4	2.1	16	48	US-10-287-822-789	0.9

16426	14.4	2.1	16	48	US-10-287-822-790	0.9
c16427	14.4	2.1	16	48	US-10-287-822-791	0.9
c16428	14.4	2.1	16	48	US-10-287-822-4210	0.9
16429	14.4	2.1	16	48	US-10-287-822-4211	0.9
c16430	14.4	2.1	16	48	US-10-287-822A-789	0.9
16431	14.4	2.1	16	48	US-10-287-822A-790	0.9
c16432	14.4	2.1	16	48	US-10-287-822A-791	0.9
c16433	14.4	2.1	16	48	US-10-287-822A-4210	0.9
16434	14.4	2.1	16	48	US-10-287-822A-4211	0.9
c63801	13.4	2	15	1	PCT-US02-25942-3193	0.893333
c63802	13.4	2	15	1	PCT-US02-25942-3705	0.893333
c63803	13.4	2	15	1	PCT-US02-25943-41284	0.893333
63804	13.4	2	15	17	US-09-274-553-2507	0.893333
63805	13.4	2	15	17	US-09-274-553B-1174	0.893333
63806	13.4	2	15	17	US-09-274-553C-1174	0.893333
63807	13.4	2	15	17	US-09-274-553D-1174	0.893333
63808	13.4	2	15	17	US-09-274-553E-1174	0.893333
63809	13.4	2	15	21	US-09-504-231A-1174	0.893333
63810	13.4	2	15	21	US-09-504-231B-1174	0.893333
63811	13.4	2	15	25	US-09-611-931-1174	0.893333
63812	13.4	2	15	25	US-09-611-931A-1174	0.893333
c63813	13.4	2	15	47	US-10-227-565-41284	0.893333
c63814	13.4	2	15	47	US-10-227-567-3193	0.893333
c63815	13.4	2	15	47	US-10-227-567-3705	0.893333
c63816	13.4	2	15	49	US-10-303-778-1347	0.893333
c63817	13.4	2	15	49	US-10-305-274-95	0.893333
c63818	13.4	2	15	49	US-10-305-274-327	0.893333
63819	13.4	2	15	49	US-10-310-188-60805	0.893333
c63820	13.4	2	15	49	US-10-316-958-71	0.893333
c63821	13.4	2	15	50	US-10-367-729A-3193	0.893333
c63822	13.4	2	15	50	US-10-367-729A-3705	0.893333
c63823	13.4	2	15	50	US-10-367-832A-41284	0.893333
7875	15	2.2	17	49	US-10-310-188-60931	0.882353
28202	14	2.1	16	49	US-10-303-778-10272	0.875
c 3	21.8	3.3	25	54	US-10-719-900-746277	0.872
c 4	21.8	3.3	25	99	US-60-427-808-746277	0.872
4786	15.4	2.3	18	49	US-10-310-188-28689	0.855556
16435	14.4	2.1	17	31	US-09-730-289B-27	0.847059
16436	14.4	2.1	17	44	US-10-061-077-79	0.847059
16437	14.4	2.1	17	44	US-10-061-077-80	0.847059
c16438	14.4	2.1	17	47	US-10-230-006-50	0.847059
c16439	14.4	2.1	17	47	US-10-230-006-547	0.847059
16440	14.4	2.1	17	49	US-10-300-683-252	0.847059
16441	14.4	2.1	17	49	US-10-310-188-24680	0.847059
16442	14.4	2.1	17	49	US-10-310-188-60661	0.847059
c16443	14.4	2.1	17	52	US-10-471-271-4464	0.847059
c16444	14.4	2.1	17	52	US-10-471-271-4734	0.847059

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
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score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						

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c 58	15.8	2.4	20	1	PCT-US04-04452-1157	0.79
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16466	11.8	1.8	15	6	US-10-781-758-5	0.786667
16467	11.8	1.8	15	6	US-10-045-674A-622	0.786667
16468	11.8	1.8	15	6	US-10-785-116-5	0.786667
169	15.2	2.3	20	6	US-10-780-439-41	0.76
170	15.2	2.3	20	6	US-10-690-276-106	0.76
171	15.2	2.3	20	6	US-10-690-276-107	0.76
4527	12.8	1.9	17	1	PCT-US03-27118-12	0.752941
59	15.8	2.4	21	1	PCT-US04-00035-9257	0.752381
16469	11.8	1.8	16	6	US-10-776-099-9	0.7375
c16470	11.8	1.8	16	6	US-10-398-483-10	0.7375
119	15.4	2.3	21	6	US-10-470-700A-36	0.733333
2815	13.2	2	18	1	PCT-US04-04452-905	0.733333
7644	12.4	1.9	17	5	US-09-941-492A-16	0.729412
1146	13.8	2.1	19	6	US-10-708-204-4501	0.726316
1147	13.8	2.1	19	6	US-10-664-668-42	0.726316
c1148	13.8	2.1	19	6	US-10-664-668-469	0.726316
1149	13.8	2.1	19	6	US-10-665-951-42	0.726316
c1150	13.8	2.1	19	6	US-10-665-951-469	0.726316
c1151	13.8	2.1	19	6	US-10-444-925A-309	0.726316
c 172	15.2	2.3	21	1	PCT-US04-00035-17210	0.72381
c52331	10.8	1.6	15	1	PCT-US04-07220-7	0.72
c52332	10.8	1.6	15	6	US-10-792-374-28	0.72
2	17.8	2.7	25	7	US-60-545-213-161396	0.712
c4528	12.8	1.9	18	6	US-10-021-698A-6079	0.711111
c 708	14.2	2.1	20	5	US-09-970-851-5	0.71
c12939	12	1.8	17	1	PCT-US03-31862-879	0.705882
12940	12	1.8	17	1	PCT-US03-31862-880	0.705882
12941	12	1.8	17	1	PCT-US03-25614-312	0.705882
12942	12	1.8	17	1	PCT-US03-25614-668	0.705882
c12943	12	1.8	17	6	US-10-488-588-9	0.705882
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c 297	14.8	2.2	21	6	US-10-770-726-6143	0.704762
c 298	14.8	2.2	21	6	US-10-770-726-7109	0.704762
c 299	14.8	2.2	21	6	US-10-770-726-7110	0.704762
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904	14	2.1	20	1	PCT-US04-04452-1268	0.7
32789	11.2	1.7	16	6	US-10-796-280-68262	0.7
c 354	14.6	2.2	21	1	PCT-US04-00035-8051	0.695238
355	14.6	2.2	21	1	PCT-US04-00035-54837	0.695238
356	14.6	2.2	21	6	US-10-770-726-3594	0.695238
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359	14.6	2.2	21	6	US-10-770-726-9390	0.695238
360	14.6	2.2	21	6	US-10-770-726-18917	0.695238
361	14.6	2.2	21	6	US-10-770-726-18918	0.695238

GenCore version 5.1.6				
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OM nucleic - nucleic search, using sw model				
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Gapop 10.0 , Gapext 1.0				
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Total number of hits satisfying chosen parameters: 78694				
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Maximum Match 100%				
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15: em_estfun:*				
16: em_estom:*				
17: em_gss_hum:*				
18: em_gss_inv:*				
19: em_gss_pln:*				
20: em_gss_vrt:*				
21: em_gss_fun:*				
22: em_gss_mam:*				

23: em_gss_mus:*						
24: em_gss_pro:*						
25: em_gss_rod:*						
26: em_gss_phg:*						
27: em_gss_vrl:*						
28: gb_gss1:*						
29: gb_gss2:*						

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

		SUMMARIES				
Result		% Query				
No.	Score	Match	Length	DB	ID	S/L
---	---	---	---	---	---	---
c7143	11.8	1.8	15	10	BE230585	0.786667
7144	11.8	1.8	15	13	BQ582543	0.786667
7145	11.8	1.8	15	13	BQ585820	0.786667
7146	11.8	1.8	15	13	BQ590410	0.786667
7147	11.8	1.8	15	13	BQ590656	0.786667
7148	11.8	1.8	15	13	BQ591170	0.786667
7149	11.8	1.8	15	13	BQ591178	0.786667
7150	11.8	1.8	15	13	BQ591223	0.786667
7151	11.8	1.8	15	13	BQ594689	0.786667
7152	11.8	1.8	15	14	CF277319	0.786667
7153	11.8	1.8	15	14	CF281923	0.786667
7154	11.8	1.8	15	14	CF290920	0.786667
7155	11.8	1.8	15	14	CF291029	0.786667
7156	11.8	1.8	15	14	CF291103	0.786667
7157	11.8	1.8	15	14	CF291717	0.786667
7158	11.8	1.8	15	14	CF291798	0.786667
7159	11.8	1.8	15	14	CF292458	0.786667
7160	11.8	1.8	15	14	CF292461	0.786667
7161	11.8	1.8	15	14	CF298148	0.786667
7162	11.8	1.8	15	14	CF298630	0.786667
7163	11.8	1.8	15	14	CF298733	0.786667
7164	11.8	1.8	15	14	CF298805	0.786667
7165	11.8	1.8	15	14	CF298889	0.786667
7166	11.8	1.8	15	14	CF299602	0.786667
7167	11.8	1.8	15	14	CF299608	0.786667
7168	11.8	1.8	15	14	CF300121	0.786667
7169	11.8	1.8	15	14	CF300361	0.786667
7170	11.8	1.8	15	14	CF300992	0.786667
7171	11.8	1.8	15	14	CF302034	0.786667
7172	11.8	1.8	15	14	CF302124	0.786667
7173	11.8	1.8	15	14	CF302182	0.786667
7174	11.8	1.8	15	14	CF307923	0.786667

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	Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model				
Run on:	March 29, 2004, 12:49:34 ; Search time 3004.06 Seconds			
	(without alignments)			
	10864.389 Million cell updates/sec			
Title:	US-09-477-082-2			
Perfect score: 753				
Sequence:	1 aattagaccgcgtattgaaa..........tacactggtttttaacctt 753			
Scoring table: IDENTITY_NUC				
	Gapop 10.0 , Gapext 1.0			
Searched:	3470272 seqs, 21671516995 residues			
Total number of hits satisfying chosen parameters:		1364278		
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
	Maximum Match 100%			
	Listing first 65000 summaries			
Database :	GenEmbl:*			
	1: gb_ba:*			
	2: gb_htg:*			
	3: gb_in:*			
	4: gb_om:*			
	5: gb_ov:*			
	6: gb_pat:*			
	7: gb_ph:*			
	8: gb_pl:*			
	9: gb_pr:*			
	10: gb_ro:*			
	11: gb_sts:*			
	12: gb_sy:*			
	13: gb_un:*			
	14: gb_vi:*			
	15: em_ba:*			
	16: em_fun:*			
	17: em_hum:*			
	18: em_in:*			
	19: em_mu:*			
	20: em_om:*			
	21: em_or:*			
	22: em_ov:*			

23: em_pat:*						
24: em_ph:*						
25: em_pl:*						
26: em_ro:*						
27: em_sts:*						
28: em_un:*						
29: em_vi:*						
30: em_htg_hum:*						
31: em_htg_inv:*						
32: em_htg_other:*						
33: em_htg_mus:*						
34: em_htg_pln:*						
35: em_htg_rod:*						
36: em_htg_mam:*						
37: em_htg_vrt:*						
38: em_sy:*						
39: em_htgo_hum:*						
40: em_htgo_mus:*						
41: em_htgo_other:*						

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	S/L
4757	14	1.9	15	6	AR231294	0.933333
c3023	14.4	1.9	16	6	A36563	0.9
3024	14.4	1.9	16	6	AR002257	0.9
3025	14.4	1.9	16	6	AR045207	0.9
3026	14.4	1.9	16	6	AR051238	0.9
c3027	14.4	1.9	16	6	AR087164	0.9
c3028	14.4	1.9	16	6	AR150597	0.9
c3029	14.4	1.9	16	6	E36063	0.9
3030	14.4	1.9	16	6	I16032	0.9
3031	14.4	1.9	16	6	I28367	0.9
c3032	14.4	1.9	16	6	I42181	0.9
c3033	14.4	1.9	16	6	I42187	0.9
c3034	14.4	1.9	16	6	I49619	0.9
c3035	14.4	1.9	16	6	AR200478	0.9
c3036	14.4	1.9	16	6	AR371265	0.9
8238	13.4	1.8	15	6	AR029856	0.893333
c8239	13.4	1.8	15	6	AR029872	0.893333
8240	13.4	1.8	15	6	AR056159	0.893333
8241	13.4	1.8	15	6	AR056160	0.893333

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Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 11:54:58 ; Search time 325.436 Seconds				
(without alignments)				
9829.571 Million cell updates/sec				
Title: US-09-477-082-2				
Perfect score: 753				
Sequence: 1 aattagaccgcgtattgaaa..........tacactggttttttaacctt 753				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 3373863 seqs, 2124099041 residues				
Total number of hits satisfying chosen parameters: 2072792				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : N_Geneseq_29Jan04:*				
1: geneseqn1980s:*				
2: geneseqn1990s:*				
3: geneseqn2000s:*				
4: geneseqn2001as:*				
5: geneseqn2001bs:*				
6: geneseqn2002s:*				
7: geneseqn2003as:*				
8: geneseqn2003bs:*				
9: geneseqn2003cs:*				
10: geneseqn2004s:*				
Pred. No. is the number of results predicted by chance to have a				
score greater than or equal to the score of the result being printed,				
and is derived by analysis of the total score distribution.				

		SUMMARIES				
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
------	------	------	------	------	------	------
6	21	2.8	21	3	AAA51822	1
c 7	21	2.8	21	3	AAA51823	1

120	18	2.4	20	9	ADE43355	0.9
3730	14.4	1.9	16	2	AAQ20008	0.9
3731	14.4	1.9	16	2	AAX18362	0.9
10799	13.4	1.8	15	2	AAQ21631	0.893333
10800	13.4	1.8	15	2	AAT00438	0.893333
10801	13.4	1.8	15	2	AAT52140	0.893333
10802	13.4	1.8	15	2	AAT52142	0.893333
10803	13.4	1.8	15	2	AAX14658	0.893333
c10804	13.4	1.8	15	2	AAX14674	0.893333
10805	13.4	1.8	15	5	AAA91455	0.893333
10806	13.4	1.8	15	5	AAA91453	0.893333
c10807	13.4	1.8	15	6	ABK54455	0.893333
10808	13.4	1.8	15	6	ABK81789	0.893333
c10809	13.4	1.8	15	7	ABZ66579	0.893333
c2080	15	2	17	9	ADE25221	0.882353
5799	14	1.9	16	2	AAX61143	0.875
15897	13	1.7	15	3	AAZ59262	0.866667
15898	13	1.7	15	4	AAF81549	0.866667
15899	13	1.7	15	4	AAF49044	0.866667
15900	13	1.7	15	4	AAF49043	0.866667
15901	13	1.7	15	4	AAF49042	0.866667
15902	13	1.7	15	5	AAH23587	0.866667
15903	13	1.7	15	6	ABA97405	0.866667
c15904	13	1.7	15	6	ABK72352	0.866667
15905	13	1.7	15	6	ABK98166	0.866667
15906	13	1.7	15	6	ABK98185	0.866667
15907	13	1.7	15	7	AAD47757	0.866667
15908	13	1.7	15	8	ADB68522	0.866667
8868	13.6	1.8	16	4	AAF82119	0.85
8869	13.6	1.8	16	5	AAH27758	0.85
8870	13.6	1.8	16	6	AAD44149	0.85
126	17.8	2.4	21	3	AAA51818	0.847619
3732	14.4	1.9	17	2	AAQ20006	0.847059
3733	14.4	1.9	17	2	AAQ20005	0.847059
3734	14.4	1.9	17	2	AAX69798	0.847059
3735	14.4	1.9	17	2	AAX69799	0.847059
3736	14.4	1.9	17	4	AAS06654	0.847059
c3737	14.4	1.9	17	7	ACC51390	0.847059
c3738	14.4	1.9	17	7	ACC51389	0.847059
c3739	14.4	1.9	17	7	ABT38540	0.847059
c3740	14.4	1.9	17	7	ADB05248	0.847059
c3741	14.4	1.9	17	7	ADB05249	0.847059
c3742	14.4	1.9	17	9	ADB42730	0.847059
c 324	16.8	2.2	20	7	ABZ77240	0.84
23979	12.6	1.7	15	3	AAA47676	0.84
23980	12.6	1.7	15	6	ABK46570	0.84
c23981	12.6	1.7	15	6	AAD26136	0.84
c23982	12.6	1.7	15	6	ABL91829	0.84
10810	13.4	1.8	16	2	AAT75139	0.8375

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OM nucleic - nucleic search, using sw model					
Run on:	March 29, 2004, 16:27:20 ; Search time 74.6121 Seconds				
	(without alignments)				
	5600.675 Million cell updates/sec				
Title:	US-09-477-082-2				
Perfect score: 753					
Sequence:	1 aattagaccgcgtattgaaa.........tacactggtttttaacctt 753				
Scoring table: IDENTITY_NUC					
	Gapop 10.0 , Gapext 1.0				
Searched:	682709 seqs, 277475446 residues				
Total number of hits satisfying chosen parameters:	718054				
Minimum DB seq length: 15					
Maximum DB seq length: 40					
Post-processing: Minimum Match 0%					
	Maximum Match 100%				
	Listing first 65000 summaries				
Database :	Issued_Patents_NA:*				
	1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*				
	2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*				
	3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*				
	4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*				
	5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*				
	6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*				
Pred. No. is the number of results predicted by chance to have a					
score greater than or equal to the score of the result being printed,					
and is derived by analysis of the total score distribution.					

		SUMMARIES				
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
---	---	---	---	---	---	---
2820	14	1.9	15	3	US-08-832-021-28	0.933333
2821	14	1.9	15	4	US-08-275-951-31	0.933333
1801	14.4	1.9	16	1	US-08-087-387-6	0.9
1802	14.4	1.9	16	1	US-08-455-627-6	0.9
c1803	14.4	1.9	16	1	US-08-283-591-16	0.9
c1804	14.4	1.9	16	1	US-08-283-591-25	0.9

c1805	14.4	1.9	16	1	US-08-088-658-34	0.9
1806	14.4	1.9	16	1	US-08-461-271-6	0.9
1807	14.4	1.9	16	1	US-08-713-685A-6	0.9
1808	14.4	1.9	16	2	US-08-689-856-6	0.9
c1809	14.4	1.9	16	2	US-08-471-907A-34	0.9
1810	14.4	1.9	16	3	US-09-070-477-6	0.9
c1811	14.4	1.9	16	3	US-08-088-661F-9	0.9
c1812	14.4	1.9	16	4	US-08-150-156A-21	0.9
c1813	14.4	1.9	16	4	US-08-108-591B-1	0.9
4872	13.4	1.8	15	1	US-08-425-315-1	0.893333
4873	13.4	1.8	15	2	US-08-292-620A-363	0.893333
4874	13.4	1.8	15	2	US-08-292-620A-364	0.893333
4875	13.4	1.8	15	2	US-08-173-489C-45	0.893333
c4876	13.4	1.8	15	2	US-08-173-489C-61	0.893333
4877	13.4	1.8	15	3	US-08-716-190-11	0.893333
4878	13.4	1.8	15	3	US-08-832-021-24	0.893333
4879	13.4	1.8	15	3	US-08-832-021-54	0.893333
4880	13.4	1.8	15	3	US-09-071-845-363	0.893333
4881	13.4	1.8	15	3	US-09-071-845-364	0.893333
2822	14	1.9	16	4	US-09-531-000-9	0.875
7116	13	1.7	15	3	US-08-832-021-25	0.866667
7117	13	1.7	15	3	US-08-832-021-26	0.866667
7118	13	1.7	15	3	US-08-832-021-27	0.866667
1814	14.4	1.9	17	4	US-08-584-040-2548	0.847059
1815	14.4	1.9	17	4	US-08-584-040-2549	0.847059
1816	14.4	1.9	17	4	US-09-371-772B-1072	0.847059
1817	14.4	1.9	17	4	US-09-371-772B-1073	0.847059
4882	13.4	1.8	16	4	US-09-124-238A-4	0.8375
4883	13.4	1.8	16	4	US-09-331-930A-4	0.8375
4884	13.4	1.8	16	4	US-09-721-975-4	0.8375
4885	13.4	1.8	16	4	US-08-894-251A-5	0.8375
4886	13.4	1.8	16	4	US-09-300-958A-56	0.8375
4887	13.4	1.8	16	4	US-09-300-958A-83	0.8375
4888	13.4	1.8	16	4	US-09-986-621-4	0.8375
4889	13.4	1.8	16	4	US-09-527-972-15	0.8375
12749	12.4	1.6	15	1	US-08-087-387-5	0.826667
12750	12.4	1.6	15	1	US-08-455-627-5	0.826667
c12751	12.4	1.6	15	1	US-08-452-196A-6	0.826667
12752	12.4	1.6	15	1	US-07-971-978-1	0.826667
12753	12.4	1.6	15	1	US-08-461-271-5	0.826667
12754	12.4	1.6	15	1	US-08-713-685A-5	0.826667
c12755	12.4	1.6	15	1	US-08-756-728A-2	0.826667
12756	12.4	1.6	15	1	US-08-663-918-3	0.826667
c12757	12.4	1.6	15	1	US-08-663-918-4	0.826667
12758	12.4	1.6	15	2	US-08-689-856-5	0.826667
12759	12.4	1.6	15	2	US-08-292-620A-9	0.826667
12760	12.4	1.6	15	2	US-08-292-620A-360	0.826667
12761	12.4	1.6	15	2	US-08-292-620A-361	0.826667
12762	12.4	1.6	15	2	US-08-292-620A-362	0.826667

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OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 18:10:30 ; Search time 291.04 Seconds				
(without alignments)				
9632.441 Million cell updates/sec				
Title: US-09-477-082-2				
Perfect score: 753				
Sequence: 1 aattagaccgcgtattgaaa.........tacactggtttttttaacctt 753				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 2458946 seqs, 1861504846 residues				
Total number of hits satisfying chosen parameters: 1244038				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : Published_Applications_NA:*				
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*				
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*				
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*				
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*				
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*				
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*				
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*				
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*				
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*				
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*				
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*				
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*				
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*				
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*				
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*				
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*				
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*				
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*				
Pred. No. is the number of results predicted by chance to have a				
score greater than or equal to the score of the result being printed,				
and is derived by analysis of the total score distribution.				

Result No.	Score	% Query Match	Length	DB	ID	S/L
		SUMMARIES				
--						
2297	14	1.9	15	14	US-10-188-404-31	0.933333
c1457	14.4	1.9	16	9	US-09-955-410-1	0.9
c1458	14.4	1.9	16	9	US-09-983-210-21	0.9
c1459	14.4	1.9	16	14	US-10-154-890-1	0.9
c4547	13.4	1.8	15	14	US-10-157-580A-142	0.893333
c 838	15	2	17	14	US-10-338-777-196	0.882353
7072	13	1.7	15	9	US-09-805-296D-12	0.866667
7073	13	1.7	15	14	US-10-072-975-12	0.866667
7074	13	1.7	15	14	US-10-051-436-12	0.866667
7075	13	1.7	15	15	US-10-360-275-12	0.866667
c 137	16.8	2.2	20	10	US-09-912-724-28	0.84
4548	13.4	1.8	16	9	US-09-811-093-21	0.8375
4549	13.4	1.8	16	9	US-09-777-422-11	0.8375
c4550	13.4	1.8	16	10	US-09-880-313A-42	0.8375
4551	13.4	1.8	16	10	US-09-997-672-30	0.8375
4552	13.4	1.8	16	10	US-09-986-625-4	0.8375
c4553	13.4	1.8	16	10	US-09-894-159-64	0.8375
4554	13.4	1.8	16	10	US-09-854-326-11	0.8375
4555	13.4	1.8	16	12	US-10-362-711-9	0.8375
4556	13.4	1.8	16	14	US-10-136-082-11	0.8375
4557	13.4	1.8	16	14	US-10-163-277-5	0.8375
4558	13.4	1.8	16	14	US-10-136-056-11	0.8375
4559	13.4	1.8	16	14	US-10-261-717-11	0.8375
4560	13.4	1.8	16	14	US-10-284-126-11	0.8375
4561	13.4	1.8	16	14	US-10-283-797-11	0.8375
4562	13.4	1.8	16	14	US-10-283-771-11	0.8375
4563	13.4	1.8	16	14	US-10-261-821-11	0.8375
c4564	13.4	1.8	16	14	US-10-164-915-2	0.8375
4565	13.4	1.8	16	14	US-10-262-258-11	0.8375
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4568	13.4	1.8	16	14	US-10-261-787-11	0.8375
4569	13.4	1.8	16	14	US-10-176-812-5	0.8375
4570	13.4	1.8	16	14	US-10-135-671-11	0.8375
4571	13.4	1.8	16	14	US-10-176-549-5	0.8375
4572	13.4	1.8	16	14	US-10-292-951-4	0.8375
4573	13.4	1.8	16	14	US-10-431-304-15	0.8375
4574	13.4	1.8	16	14	US-10-283-874-11	0.8375
4575	13.4	1.8	16	15	US-10-362-262-3	0.8375
c14381	12.4	1.6	15	9	US-09-817-387-22	0.826667
14382	12.4	1.6	15	9	US-09-504-231A-22	0.826667
c14383	12.4	1.6	15	9	US-09-504-231A-1175	0.826667

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
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(without alignments)				
9153.537 Million cell updates/sec				
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Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 37577330 seqs, 17593059518 residues				
Total number of hits satisfying chosen parameters: 26876998				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	21	2.8	21	20	US-09-477-082-33	1
c 7	21	2.8	21	20	US-09-477-082-34	1
c 20	20	2.7	20	48	US-10-293-338-2237	1

c8917	15	2	15	1	PCT-US02-25944-4476	1
c8918	15	2	15	1	PCT-US02-25944-4488	1
c8919	15	2	15	47	US-10-227-564-4476	1
c8920	15	2	15	47	US-10-227-564-4488	1
c2269	16	2.1	17	49	US-10-310-188-24893	0.941176
31751	14	1.9	15	1	PCT-US02-25944-2473	0.933333
31752	14	1.9	15	1	PCT-US02-25944-2498	0.933333
31753	14	1.9	15	46	US-10-188-404-31	0.933333
31754	14	1.9	15	47	US-10-227-564-2473	0.933333
31755	14	1.9	15	47	US-10-227-564-2498	0.933333
c31756	14	1.9	15	49	US-10-305-273-37	0.933333
c31757	14	1.9	15	49	US-10-305-273A-37	0.933333
c31758	14	1.9	15	49	US-10-305-273B-37	0.933333
c 510	17.4	2.3	19	49	US-10-310-188-24640	0.915789
c 511	17.4	2.3	19	49	US-10-310-188-60701	0.915789
c 512	17.4	2.3	19	49	US-10-310-188-72940	0.915789
5273	15.4	2	17	27	US-09-653-225-1416	0.905882
5274	15.4	2	17	54	US-10-712-672-1416	0.905882
270	18	2.4	20	1	PCT-US02-34679-524	0.9
271	18	2.4	20	48	US-10-282-174-524	0.9
272	18	2.4	20	53	US-10-600-009-524	0.9
18606	14.4	1.9	16	1	PCT-US94-07557-6	0.9
18607	14.4	1.9	16	4	US-08-087-386B-6	0.9
18608	14.4	1.9	16	7	US-08-359-295A-10	0.9
c18609	14.4	1.9	16	8	US-08-462-977-1	0.9
c18610	14.4	1.9	16	8	US-08-462-977B-1	0.9
c18611	14.4	1.9	16	8	US-08-468-719-1	0.9
c18612	14.4	1.9	16	8	US-08-468-719A-1	0.9
c18613	14.4	1.9	16	12	US-08-817-067-152	0.9
c18614	14.4	1.9	16	12	US-08-817-067A-152	0.9
c18615	14.4	1.9	16	20	US-09-442-054-34	0.9
c18616	14.4	1.9	16	20	US-09-442-054A-34	0.9
c18617	14.4	1.9	16	40	US-09-955-410-1	0.9
c18618	14.4	1.9	16	42	US-09-983-210-21	0.9
c18619	14.4	1.9	16	46	US-10-154-890-1	0.9
c18620	14.4	1.9	16	48	US-10-287-787-25195	0.9
c2270	16	2.1	18	49	US-10-310-188-83566	0.888889
c8921	15	2	17	49	US-10-310-188-83556	0.882353
c8922	15	2	17	49	US-10-338-777-196	0.882353
c31759	14	1.9	16	49	US-10-303-778-14428	0.875
c31760	14	1.9	16	49	US-10-310-188-26546	0.875
c 513	17.4	2.3	20	48	US-10-293-338-4193	0.87
514	17.4	2.3	20	49	US-10-310-188-1921	0.87
1540	16.4	2.2	19	48	US-10-287-787-25194	0.863158
1541	16.4	2.2	19	49	US-10-310-188-64693	0.863158
5275	15.4	2	18	49	US-10-310-188-9840	0.855556
c5276	15.4	2	18	49	US-10-310-188-14825	0.855556

GenCore version 5.1.6					
Copyright (c) 1993 - 2004 Compugen Ltd.					
OM nucleic - nucleic search, using sw model					
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Pred. No. is the number of results predicted by chance to have a					
score greater than or equal to the score of the result being printed,					
and is derived by analysis of the total score distribution.					

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		%				
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28	16.8	2.2	20	6	US-10-690-276-174	0.84
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8186	12.4	1.6	15	6	US-10-781-758-5	0.826667
8187	12.4	1.6	15	6	US-10-045-674A-622	0.826667
8188	12.4	1.6	15	6	US-10-456-982-8	0.826667

8189	12.4	1.6	15	6	US-10-785-116-5	0.826667
c1329	13.8	1.8	17	1	PCT-US03-25614-376	0.811765
285	15	2	19	6	US-10-708-204-5035	0.789474
17660	11.8	1.6	15	6	US-10-788-232-132	0.786667
8190	12.4	1.6	16	6	US-10-776-099-9	0.775
c8191	12.4	1.6	16	6	US-10-398-483-10	0.775
c 46	16.2	2.2	21	1	PCT-US04-00035-23548	0.771429
c 47	16.2	2.2	21	6	US-10-786-720-6011	0.771429
135	15.4	2	20	6	US-10-667-275A-7	0.77
195	15.2	2	20	1	PCT-US04-04205-2	0.76
196	15.2	2	20	1	PCT-US04-04452-770	0.76
197	15.2	2	20	6	US-10-777-838-2	0.76
198	15.2	2	20	6	US-10-789-113-3	0.76
199	15.2	2	20	6	US-10-789-113-4	0.76
c 200	15.2	2	20	6	US-10-476-021-97	0.76
4842	12.8	1.7	17	6	US-10-398-445-51	0.752941
807	14.2	1.9	19	1	PCT-US03-35072-23	0.747368
808	14.2	1.9	19	6	US-10-387-346B-154	0.747368
c 809	14.2	1.9	19	6	US-10-664-668-173	0.747368
810	14.2	1.9	19	6	US-10-664-668-600	0.747368
c 811	14.2	1.9	19	6	US-10-665-951-173	0.747368
812	14.2	1.9	19	6	US-10-665-951-600	0.747368
c17661	11.8	1.6	16	6	US-10-708-204-4602	0.7375
17662	11.8	1.6	16	6	US-10-647-982A-18	0.7375
c17663	11.8	1.6	16	6	US-10-661-165-203	0.7375
1003	14	1.9	19	6	US-10-664-668-246	0.736842
c1004	14	1.9	19	6	US-10-664-668-673	0.736842
1005	14	1.9	19	6	US-10-665-951-246	0.736842
c1006	14	1.9	19	6	US-10-665-951-673	0.736842
c 136	15.4	2	21	1	PCT-US04-00035-22644	0.733333
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3128	13.2	1.8	18	6	US-10-653-416-26	0.733333
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45580	11	1.5	15	6	US-10-488-619-1683	0.733333
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c8192	12.4	1.6	17	1	PCT-US03-31862-1339	0.729412
8193	12.4	1.6	17	1	PCT-US03-31862-1340	0.729412
8194	12.4	1.6	17	1	PCT-US03-31862-2075	0.729412
c8195	12.4	1.6	17	1	PCT-US03-31862-2076	0.729412
c8196	12.4	1.6	17	1	PCT-US04-06948-25	0.729412
201	15.2	2	21	1	PCT-US04-00035-2986	0.72381
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203	15.2	2	21	1	PCT-US04-00035-9756	0.72381
c 204	15.2	2	21	1	PCT-US04-00035-23070	0.72381
205	15.2	2	21	1	PCT-US04-00035-31098	0.72381
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GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
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	Maximum Match 100%			
	Listing first 65000 summaries			
Database :	EST:*			
	1: em_estba:*			
	2: em_esthum:*			
	3: em_estin:*			
	4: em_estmu:*			
	5: em_estov:*			
	6: em_estpl:*			
	7: em_estro:*			
	8: em_htc:*			
	9: gb_est1:*			
	10: gb_est2:*			
	11: gb_htc:*			
	12: gb_est3:*			
	13: gb_est4:*			
	14: gb_est5:*			
	15: em_estfun:*			
	16: em_estom:*			
	17: em_gss_hum:*			
	18: em_gss_inv:*			
	19: em_gss_pln:*			
	20: em_gss_vrt:*			
	21: em_gss_fun:*			
	22: em_gss_mam:*			

23: em_gss_mus:*				,	
24: em_gss_pro:*					
25: em_gss_rod:*					
26: em_gss_phg:*					
27: em_gss_vrl:*					
28: gb_gss1:*					
29: gb_gss2:*					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		SUMMARIES				
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
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c4962	13	1.7	15	14	CF543203	0.866667
c3920	13.4	1.8	16	14	CF291803	0.8375
510	15.8	2.1	19	28	AZ645841	0.831579
96	17.4	2.3	21	28	AZ647578	0.828571
c6707	12.4	1.6	15	10	BE230585	0.826667
6708	12.4	1.6	15	13	BQ582543	0.826667
6709	12.4	1.6	15	13	BQ585820	0.826667
6710	12.4	1.6	15	13	BQ590410	0.826667
6711	12.4	1.6	15	13	BQ590656	0.826667
6712	12.4	1.6	15	13	BQ591170	0.826667
6713	12.4	1.6	15	13	BQ591178	0.826667
6714	12.4	1.6	15	13	BQ591223	0.826667
6715	12.4	1.6	15	13	BQ594689	0.826667
6716	12.4	1.6	15	14	CF277319	0.826667
6717	12.4	1.6	15	14	CF281923	0.826667
c6718	12.4	1.6	15	14	CF290849	0.826667
6719	12.4	1.6	15	14	CF290920	0.826667
6720	12.4	1.6	15	14	CF291029	0.826667
6721	12.4	1.6	15	14	CF291103	0.826667
6722	12.4	1.6	15	14	CF291717	0.826667
6723	12.4	1.6	15	14	CF291798	0.826667
6724	12.4	1.6	15	14	CF292458	0.826667
6725	12.4	1.6	15	14	CF292461	0.826667
6726	12.4	1.6	15	14	CF295100	0.826667
6727	12.4	1.6	15	14	CF296652	0.826667
6728	12.4	1.6	15	14	CF298148	0.826667
6729	12.4	1.6	15	14	CF298630	0.826667
6730	12.4	1.6	15	14	CF298733	0.826667
6731	12.4	1.6	15	14	CF298805	0.826667
6732	12.4	1.6	15	14	CF298889	0.826667
6733	12.4	1.6	15	14	CF299602	0.826667

presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM7 row: D column: 12
High quality sequence stop: 14.

FEATURES   Location/Qualifiers
source   1..15
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:2821595"
         /tissue_type="small cell carcinoma"
         /cell_line="MGC3"
         /lab_host="DH10B (phage-resistant)"
         /clone_lib="NIH_MGC_7"
         /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
         EcoRI; cDNA made by oligo-dT priming. Directionally
         cloned into EcoRI/XhoI sites using the following 5'
         adaptor: GGCACGAG(G). Size-selected >500bp for average
         insert size 1.8kb. Library constructed by Ling Hong in
         the laboratory of Gerald M. Rubin (University of
         California, Berkeley) using ZAP-cDNA synthesis kit
         (Stratagene) and Superscript II RT (Life Technologies)."

Query Match   1.2%;   Score 9.2;   DB 1;   Length 15;
Best Local Similarity   78.6%;   Pred. No. 0;
Matches   11;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   638 TGCCCAAAAAACAA 651
         || ||||||||| ||
Db   15 TGATCAAAAAAAAA 2

Search completed: March 31, 2004, 14:14:07
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:14:07 ; Search time 0.001 Seconds
                   (without alignments)
                   22.590 Million cell updates/sec

Title: us09477082Z
Perfect score: 753
Sequence: 1 aattagaccggtattgaaa.............tacactggtttttaacctt 753

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 15 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 100 summaries

Database :   2rsrt.db:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                                 SUMMARIES

Result   %   Query
  No.   Score   Match Length DB ID   Description
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c   1   14   1.9   15   1   AW246494   ACCESSION:AW246494
c   2   9.2   1.2   15   1   AW246494   ACCESSION:AW246494

                               ALIGNMENTS

RESULT 1
LOCUS   AW246494   15 bp   mRNA   linear   EST 07-JAN-2000
DEFINITION 2821595.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821595 3',
            mRNA sequence.
ACCESSION   AW246494
VERSION   AW246494.1 GI:6589487
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: 2821595.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector

Qy   717 TTTTTTTTTTGATC 730
           |||||||||||||||
Db   1 TTTTTTTTTTGATC 14

Query Match   1.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821595"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
     High quality sequence stop: 14.
                     Plate: LLCM7 row: D column: 12
                     High quality sequence start: 1..15

COMMENT   Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 14
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 15 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.

RESULT 2
AW246494/c
LOCUS   AW246494   15 bp   mRNA   linear   EST 07-JAN-2000
DEFINITION 2821595.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821595 3',
            mRNA sequence.
ACCESSION   AW246494
VERSION   AW246494.1 GI:6589487
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: 2821595.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Very
            Low Quality Sequence: Trace file contained 15 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
;   DOCUMENT NUMBER: WO PCT/EP92/01220
;   FILING DATE: 22-MAY-1992
US-09-983-210-21

Qy          640 CCCAAAAAACAAG 652
                |||||||| |||
Db            4 CCAAAAAAAAAG 16

Query Match             1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity  84.6%;  Pred. No. 6.7;
Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

RESULT 7
US-10-154-890-1
Sequence 1, Application US/10154890
Publication No. US20030180734A1
GENERAL INFORMATION:
;   APPLICANT: Buchardt, Ole
;   APPLICANT: Egholm, Michael
;   APPLICANT: Nielsen, Peter Eigil
;   APPLICANT: Berg, Rolf Henrik
;   TITLE OF INVENTION: Peptide Nucleic Acids
;   FILE REFERENCE: ISIS0540
;   CURRENT APPLICATION NUMBER: US/10/154,890
;   CURRENT FILING DATE: 2002-05-23
;   PRIOR APPLICATION NUMBER: US/08/108,591
;   PRIOR FILING DATE: 2001-08-13
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030180734A1e1 Sequence
US-10-154-890-1

Qy          640 CCCAAAAAACAAG 652
                |||||||| |||
Db            4 CCAAAAAAAAAG 16

Query Match             1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity  84.6%;  Pred. No. 6.7;
Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

RESULT 8
US-10-188-404-31/c
Sequence 31, Application US/10188404
Publication No. US20030105286A1
GENERAL INFORMATION:
;   APPLICANT: Egholm, Michael
;   APPLICANT: Neilsen, Peter
;   APPLICANT: Buchardt, Ole
;   APPLICANT: Dueholm, Kim L.
;   APPLICANT: Christensen, Leif
;   APPLICANT: Coull, James M.
;   APPLICANT: Kiely, John
;   APPLICANT: Griffith, Michael
;   TITLE OF INVENTION: Linked Peptide Nucleic Acids
;   FILE REFERENCE: ISIS5042
;   CURRENT APPLICATION NUMBER: US/10/188,404
;   CURRENT FILING DATE: 2002-07-01
;   PRIOR APPLICATION NUMBER: 08/275,951
;   PRIOR FILING DATE: 1994-07-15
;   PRIOR APPLICATION NUMBER: 08/765,798
;   PRIOR FILING DATE: 1997-04-23
;   NUMBER OF SEQ ID NOS: 69
;   SOFTWARE: Patentin version 3.1
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; SEQ ID NO 31
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(7)
;   OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
;   OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-31

Qy          18 AAAGTAAAAGAA 29
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Db          14 AAAGAAAAAAA  3

Query Match             1.2%;  Score 8.8;  DB 1;  Length 15;
Best Local Similarity  83.3%;  Pred. No. 8.1;
Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Search completed: March 31, 2004, 14:11:57
Job time : 0.001 secs
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; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/10/154,890
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1e1 Sequence
US-10-154-890-1

Qy   715 CTTTTTTTTTTGATC 730
           ||||||||||||||||
Db   16 CTTTTTTTTTTGGATC 1

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No.1.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
US-10-188-404-31
; Sequence 31, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Buchardt, Ole
; APPLICANT: Nielsen, Peter
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
; OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-31

Query Match   1.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   460 CTTTTTTTTCTTTT 473
           ||||||||||||||
Db   2 CTTTTTTTTCTTTT 15

RESULT 5
US-09-955-410-1
; Sequence 1, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS4800
; CURRENT APPLICATION NUMBER: US/09/955,410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020146718A1e1 Sequence
US-09-955-410-1

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Best Local Similarity 84.6%; Pred. No. 6.7;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   640 CCCAAAAAACAAG 652
           || ||||||| |||
Db   4 CCAAAAAAAAAG 16

RESULT 6
US-09-983-210-21
; Sequence 21, Application US/09983210
; Patent No. US20020160383A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,210
; FILING DATE: 2001-Oct-23
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: March 31, 2004, 14:11:57 ; Search time 0.001 Seconds
                                      (without alignments)
                                      94.878 Million cell updates/sec

Title: us09470822
Perfect score: 753
Sequence: 1 aattagaccgtattgaaa..............tacactggttcttaacctt 753

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched: 4 segs, 63 residues

Total number of hits satisfying chosen parameters: 8

Minimum Match 0%
Maximum Match 100%
                Listing first 50 summaries

Database : 2rnpb.db:*

Post-processing: Minimum Match 0%
Maximum Match 100%
                Listing first 50 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : 2rnpb.db:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.4	1.9	16	1	US-09-955-410-1	Sequence 1, Appli
2	14.4	1.9	16	1	US-09-983-210-21	Sequence 21, Appl
3	14.4	1.9	16	1	US-10-154-890-1	Sequence 1, Appl
4	14	1.9	15	1	US-10-188-404-31	Sequence 31, Appl
5	9.8	1.3	16	1	US-09-955-410-1	Sequence 1, Appl
6	9.8	1.3	16	1	US-09-983-210-21	Sequence 21, Appl
7	9.8	1.3	16	1	US-10-154-890-1	Sequence 1, Appl
8	8.8	1.2	15	1	US-10-188-404-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-955-410-1/c
; Sequence 1, Application US/0995410
; Patent No. US2002014671BAl
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: IST54800
; CURRENT APPLICATION NUMBER: US/09/955,410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1

; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US2002014671BAle1 Sequence
US-09-955-410-1

Qy   715 CTTTTTTTTTGATC 730
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Db   16 CTTTTTTTTTGGATC 1

Query Match   1.9%;   Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%;   Pred. No. 1.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
US-09-983-210-21/c
; Sequence 21, Application US/0983210
; Patent No. US2002016038AAl
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,210
; FILING DATE: 2001-OCT-23
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-09-983-210-21

Qy   715 CTTTTTTTTTGATC 730
           |||||||||||||| ||||
Db   16 CTTTTTTTTTGGATC 1

Query Match   1.9%;   Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%;   Pred. No. 1.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
US-10-154-890-1/c
; Sequence 1, Application US/10154890
; Publication No. US2003018073AAl
; GENERAL INFORMATION:

; TOPOLOGY: linear
US-09-070-477-6

Query Match   1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity   90.9%; Pred. No. 26;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   643 AAAAAACAAGT 653
            |||||||| |||
Db   11 AAAAAAAAAGT 1

RESULT 29
US-08-275-951-31/c
Sequence 31, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS1577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 64519681 Sequence
; NAME/KEY: misc_feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
; OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-31

Query Match   1.2%; Score 8.8; DB 1; Length 15;
Best Local Similarity   83.3%; Pred. No. 30;
Matches   10; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   18 AAAGTAAAAGAA 29
            ||| |||||||
Db   14 AAAGAAAAAAA 3

RESULT 30
US-08-832-021-28/c
Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

Query Match   1.1%; Score 8.4; DB 1; Length 15;
Best Local Similarity   90.0%; Pred. No. 31;
Matches   9; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   642 CAAAAAACAA 651
            ||||||| ||
Db   13 CAAAAAAAAA 4

Search completed: March 31, 2004, 14:10:54
Job time : 0.001 secs

~ APPLICANT: Sergei M. Gryaznov
~ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
~   and therapeutic applications
~ NUMBER OF SEQUENCES: 6
~ CORRESPONDENCE ADDRESS:
~ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
~ STREET: 465 Lincoln Centre Drive
~ CITY: Foster City
~ STATE: California
~ COUNTRY: USA
~ ZIP: 94404
~ COMPUTER READABLE FORM:
~ MEDIUM TYPE: 5.25 inch diskette
~ COMPUTER: IBM compatible
~ OPERATING SYSTEM: Windows 3.1/DOS 5.0
~ SOFTWARE: Microsoft Word for Windows, vers. 2.0
~ CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/08/713,685A
~ FILING DATE:
~ CLASSIFICATION:
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER: 08/461,271
~ FILING DATE:
~ APPLICATION NUMBER: 08/087,387
~ FILING DATE: 2-Jul-93
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Stephen C. Macevicz
~ REGISTRATION NUMBER: 30,285
~ REFERENCE/DOCKET NUMBER: 104
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: (415) 358-7855
~ TELEFAX: (415) 358-7794
~ INFORMATION FOR SEQ ID NO: 6:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 16 nucleotides
~ TYPE: nucleic acid
~ STRANDEDNESS: single
~ TOPOLOGY: linear
~ US-08-713-685A-6

Qy   643 AAAAAACAAGT 653
          |||||||| ||||
Db   11 AAAAAAAAGT 1

Query Match   1.2%;   Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-08-689-856-6

RESULT 27
US-08-689-856-6/c
Sequence 6, Application US/08689856
Patent No. 5830658
GENERAL INFORMATION:
~ APPLICANT: Sergei M. Gryaznov
~ TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
~   Connected Macromolecular Structures
~ NUMBER OF SEQUENCES: 26
~ CORRESPONDENCE ADDRESS:
~ ADDRESSEE: Cooley Godward LLP
~ STREET: Five Palo Alto Square, 3000 El Camino Real
~ CITY: Palo Alto
~ STATE: California
~ COUNTRY: USA
~ ZIP: 94306-2155
~ COMPUTER READABLE FORM:
~ MEDIUM TYPE: Floppy disk
~ COMPUTER: IBM PC compatible
~ OPERATING SYSTEM: PC-DOS/MS-DOS
~ SOFTWARE: PatentIn Release #1.0, Version #1.25
~ CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/08/689,856
~ FILING DATE:

~ CLASSIFICATION:
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER: US/08/455,627
~ FILING DATE: 31-MAY-1995
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Nakamura, Jackie N.
~ REGISTRATION NUMBER: 35,966
~ REFERENCE/DOCKET NUMBER: LYNX-003/01 US
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: 415-843-5000
~ TELEFAX: 415-857-0663
~ INFORMATION FOR SEQ ID NO: 6:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 16 nucleotides
~ TYPE: nucleic acid
~ STRANDEDNESS: single
~ TOPOLOGY: linear
~ MOLECULE TYPE: DNA
~ US-08-689-856-6

Qy   643 AAAAAACAAGT 653
          |||||||| ||||
Db   11 AAAAAAAAGT 1

Query Match   1.2%;   Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-070-477-6/c

RESULT 28
US-09-070-477-6/c
Sequence 6, Application US/09070477
Patent No. 6048974
GENERAL INFORMATION:
~ APPLICANT: Sergei M. Gryaznov
~ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
~   and therapeutic applications
~ NUMBER OF SEQUENCES: 6
~ CORRESPONDENCE ADDRESS:
~ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
~ STREET: 465 Lincoln Centre Drive
~ CITY: Foster City
~ STATE: California
~ COUNTRY: USA
~ ZIP: 94404
~ COMPUTER READABLE FORM:
~ MEDIUM TYPE: 5.25 inch diskette
~ COMPUTER: IBM compatible
~ OPERATING SYSTEM: Windows 3.1/DOS 5.0
~ SOFTWARE: Microsoft Word for Windows, vers. 2.0
~ CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/09/070,477
~ FILING DATE:
~ CLASSIFICATION:
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER: US/08/713,685
~ FILING DATE:
~ APPLICATION NUMBER: 08/461,271
~ FILING DATE:
~ APPLICATION NUMBER: 08/087,387
~ FILING DATE: 2-Jul-93
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Stephen C. Macevicz
~ REGISTRATION NUMBER: 30,285
~ REFERENCE/DOCKET NUMBER: 104
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: (415) 358-7855
~ TELEFAX: (415) 358-7794
~ INFORMATION FOR SEQ ID NO: 6:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 16 nucleotides
~ TYPE: nucleic acid
~ STRANDEDNESS: single

```
                STATE: California
                COUNTRY: USA
                ZIP: 94404
          COMPUTER READABLE FORM:
                MEDIUM TYPE: 5.25 inch diskette
                COMPUTER: IBM compatible
                OPERATING SYSTEM: Windows 3.1/DOS 5.0
                SOFTWARE: Microsoft Word for Windows, vers. 2.0
          CURRENT APPLICATION DATA:
                APPLICATION NUMBER: 435
                FILING DATE: 19930702
                CLASSIFICATION: 435
          PRIOR APPLICATION DATA:
                APPLICATION NUMBER: US/08/087,387
                FILING DATE:
                APPLICATION NUMBER:
          ATTORNEY/AGENT INFORMATION:
                NAME: Stephen C. Macevicz
                REGISTRATION NUMBER: 30,285
                REFERENCE/DOCKET NUMBER: 104
          TELECOMMUNICATION INFORMATION:
                TELEPHONE: (415) 358-7855
                TELEFAX: (415) 358-7794
     INFORMATION FOR SEQ ID NO: 6:
          SEQUENCE CHARACTERISTICS:
                LENGTH: 16 nucleotides
                TYPE: nucleic acid
                STRANDEDNESS: single
                TOPOLOGY: linear
US-08-087-387-6

Query Match            1.2%;  Score 9.4; DB 1; Length 16;
Best Local Similarity  90.9%; Pred. No. 26;
Matches 10; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

Qy    643 AAAAACAAGT 653
          ||||||| ||||
Db     11 AAAAAAAAGT 1

RESULT 24
US-08-455-627-6/c
Sequence 6, Application US/08455627
Patent No. 5571677
GENERAL INFORMATION:
     APPLICANT: Sergei M. Gryaznov
     TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
     TITLE OF INVENTION: Connected Macromolecular Structures
     NUMBER OF SEQUENCES: 26
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Cooley Godward LLP
          STREET: Five Palo Alto Square, 3000 El Camino Real
          CITY: Palo Alto
          STATE: California
          COUNTRY: USA
          ZIP: 94306-2155
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/08/455,627
          FILING DATE: 31-MAY-1995
          CLASSIFICATION: 435
     ATTORNEY/AGENT INFORMATION:
          NAME: Nakamura, Jackie N.
          REGISTRATION NUMBER: 35,966
          REFERENCE/DOCKET NUMBER: LYNX-003/01 US
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: 415-843-5000
          TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 6:
     SEQUENCE CHARACTERISTICS:
```

```
          LENGTH: 16 nucleotides
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
          MOLECULE TYPE: DNA
US-08-455-627-6

Qy    643 AAAAACAAGT 653
          ||||||| ||||
Db     11 AAAAAAAAGT 1

Query Match            1.2%;  Score 9.4; DB 1; Length 16;
Best Local Similarity  90.9%; Pred. No. 26;
Matches 10; Conservative  0; Mismatches  1; Indels  0; Gaps  0;
US-08-455-627-6

RESULT 25
US-08-461-271-6/c
Sequence 6, Application US/08461271
Patent No. 5741643
GENERAL INFORMATION:
     APPLICANT: Sergei M. Gryaznov
     TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
     TITLE OF INVENTION: and therapeutic applications
     NUMBER OF SEQUENCES: 6
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
          STREET: 465 Lincoln Centre Drive
          CITY: Foster City
          STATE: California
          COUNTRY: USA
          ZIP: 94404
     COMPUTER READABLE FORM:
          MEDIUM TYPE: 5.25 inch diskette
          COMPUTER: IBM compatible
          OPERATING SYSTEM: Windows 3.1/DOS 5.0
          SOFTWARE: Microsoft Word for Windows, vers. 2.0
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/08/461,271
          FILING DATE:
          CLASSIFICATION: 435
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 08/087,387
          FILING DATE: 2-Jul-93
     ATTORNEY/AGENT INFORMATION:
          NAME: Stephen C Macevicz
          REGISTRATION NUMBER: 30,285
          REFERENCE/DOCKET NUMBER: 104
     TELECOMMUNICATION INFORMATION:
          TELEPHONE: (415) 358-7855
          TELEFAX: (415) 358-7794
     INFORMATION FOR SEQ ID NO: 6:
          SEQUENCE CHARACTERISTICS:
          LENGTH: 16 nucleotides
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
US-08-461-271-6

Query Match            1.2%;  Score 9.4; DB 1; Length 16;
Best Local Similarity  90.9%; Pred. No. 26;
Matches 10; Conservative  0; Mismatches  1; Indels  0; Gaps  0;

Qy    643 AAAAACAAGT 653
          ||||||| ||||
Db     11 AAAAAAAAGT 1

RESULT 26
US-08-713-685A-6/c
Sequence 6, Application US/08713685A
Patent No. 5817795
GENERAL INFORMATION:
```

```
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-907A-34

Qy  640 CCCAAAAAACAAG 652
        |||||||||| |||
Db    4 CCAAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;  Pred. No. 25;
Matches 11;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

RESULT 20
US-08-088-661F-9
; Sequence 9, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
; APPLICANT: NO. 6228982den, Benget
; APPLICANT: Wittung, Pernilla
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982e1 Sequence
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
; FILE REFERENCE: I:S1108
; CURRENT APPLICATION NUMBER: US/08/088,661F
; CURRENT FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19

RESULT 21
US-08-150-156A-21
; Sequence 21, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0966/91
; FILING DATE: 24-MAY-1991
; TITLE OF INVENTION:  THE USE OF NUCLEIC ACID ANALOGUES IN
;   DIAGNOSTICS AND ANALYTICAL PROCEDURES

Qy  640 CCCAAAAAACAAG 652
        |||||||||| |||
Db    4 CCAAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;  Pred. No. 25;
Matches 11;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
US-08-088-661F-9

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-21

Qy  640 CCCAAAAAACAAG 652
        |||||||||| |||
Db    4 CCAAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;  Pred. No. 25;
Matches 11;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

RESULT 22
US-08-108-591B-1
; Sequence 1, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf Henrik
; APPLICANT: Berg, Peter Eigil
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: I:S0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474e1 Sequence
US-08-108-591B-1

Qy  640 CCCAAAAAACAAG 652
        |||||||||| |||
Db    4 CCAAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;  Pred. No. 25;
Matches 11;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

RESULT 23
US-08-087-387-6/c
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
```

```
    TITLE OF INVENTION: NOVEL TRISUBSTITUTED  -LACTAMS AND
    TITLE OF INVENTION: OLIGO  -LACTAMAMIDES
    NUMBER OF SEQUENCES: 28
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
    ADDRESSEE: No. 562915zris
    STREET: One Liberty Place - 46th Floor
    CITY: Philadelphia
    STATE: PA
    COUNTRY: U.S.A.
    ZIP: 19103
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/283,591
    FILING DATE: N/A
    CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
    ATTORNEY/AGENT INFORMATION:
    NAME:
    REGISTRATION NUMBER:
    REFERENCE/DOCKET NUMBER:
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: 215-568-3100
    TELEFAX: 215-568-3439
  INFORMATION FOR SEQ ID NO: 25:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 16
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: unknown
  US-08-283-591-25

Qy      640 CCCAAAAAACAAG 652
            |||||||  |||
Db        4 CCAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8; DB 1; Length 16;
Best Local Similarity    84.6%;  Pred. No. 25;
Matches   11;  Conservative   0; Mismatches   2; Indels   0; Gaps   0;
```

```
RESULT 18
US-08-088-658-34
; Sequence 34, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
;   APPLICANT: Ecker, David J.
;   APPLICANT: Buchardt, Ole
;   APPLICANT: Egholm, Michael
;   APPLICANT: Nielsen, Peter E.
;   APPLICANT: Berg, Rolf H.
;   APPLICANT: M llegaard, Niels E.
;   TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
;   TITLE OF INVENTION: NUCLEIC ACIDS
;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
;     STREET: One Liberty Place - 46th Floor
;     CITY: Philadelphia
;     STATE: PA
;     COUNTRY: U.S.A.
;     ZIP: 19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/088,658
      FILING DATE: 19930702
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/054,363
      FILING DATE: 26-APRIL-1993
    ATTORNEY/AGENT INFORMATION:
      NAME: Lucci, Joseph
      REGISTRATION NUMBER: 33,307
      REFERENCE/DOCKET NUMBER: ISIS-1052
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 215-568-3100
      TELEFAX: 215-568-3439
  INFORMATION FOR SEQ ID NO: 34:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 16
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
  US-08-088-658-34

Qy      640 CCCAAAAAACAAG 652
            |||||||  |||
Db        4 CCAAAAAAAAAG 16

Query Match       1.3%;  Score 9.8; DB 1; Length 16;
Best Local Similarity    84.6%;  Pred. No. 25;
Matches   11;  Conservative   0; Mismatches   2; Indels   0; Gaps   0;
```

```
RESULT 19
US-08-471-907A-34
; Sequence 34, Application US/08471907A
; Patent No. 5986053
; GENERAL INFORMATION:
;   APPLICANT: Ecker, David J.
;   APPLICANT: Buchardt, Ole
;   APPLICANT: Egholm, Michael
;   APPLICANT: Nielsen, Peter E.
;   APPLICANT: Berg, Rolf H.
;   APPLICANT: M llegaard, Niels E.
;   TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
;   TITLE OF INVENTION: NUCLEIC ACIDS
;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
;     STREET: One Liberty Place - 46th Floor
;     CITY: Philadelphia
;     STATE: PA
;     COUNTRY: U.S.A.
;     ZIP: 19103
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/471,907A
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/088,658
      FILING DATE:
    ATTORNEY/AGENT INFORMATION:
      NAME: Lucci, Joseph
      REGISTRATION NUMBER: 33,307
      REFERENCE/DOCKET NUMBER: ISIS-1052
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 215-568-3100
      TELEFAX: 215-568-3439
  INFORMATION FOR SEQ ID NO: 34:
    SEQUENCE CHARACTERISTICS:
```

RESULT 14
US-08-832-021-28
; Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

Qy   716 TTTTTTTTTTTTGAT 729
                |||||||||||||||
Db   2 TTTTTTTTTTTTGAT 15

Query Match   1.9%; Score 14; DB 1; Length 15;
Best Local Similarity   100.0%; Pred. No. 5.6;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 15
US-08-275-951-31
; Sequence 31, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS1577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; NAME/KEY: misc_feature

; LOCATION: (6)..(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
; OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-31

Qy   460 CTTTTTTTTCTTTT 473
                ||||||||||||||
Db   2 CTTTTTTTTCTTTT 15

Query Match   1.9%; Score 14; DB 1; Length 15;
Best Local Similarity   100.0%; Pred. No. 5.6;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 16
US-08-283-591-16
; Sequence 16, Application US/08283591
; Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; TITLE OF INVENTION: NOVEL TRISUBSTITUTED   -LACTAMS AND
; TITLE OF INVENTION: OLIGO   -LACTAMIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5629152rl8
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,591
; FILING DATE: N/A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-283-591-16

Qy   640 CCCAAAAAACAAG 652
                ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

Query Match   1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity   84.6%; Pred. No. 25;
Matches   11; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT 17
US-08-283-591-25
; Sequence 25, Application US/08283591
; Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga

```
;        FILING DATE:
;        APPLICATION NUMBER: 08/087,387
;        FILING DATE: 2-Jul-93
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Stephen C. Macevicz
;        REGISTRATION NUMBER: 30,285
;        REFERENCE/DOCKET NUMBER: 104
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (415) 358-7855
;        TELEFAX: (415) 358-7794
;  INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 16 nucleotides
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
US-09-070-477-6

Qy      459 ACTTTTTTTTCTTTTT 474
            ||||||||| |||||||
Db        1 ACTTTTTTTTTTTTTTT 16

Query Match       1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity   93.8%;  Pred. No. 4.3;
Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

RESULT 11
US-08-088-661F-9/c
Sequence 9, Application US/08088661F
Patent No. 6228982
GENERAL INFORMATION:
   APPLICANT: No. 6228982den, Benget
   APPLICANT: Wittung, Pernilla
   APPLICANT: Buchardt, Ole
   APPLICANT: Egholm, Michael
   APPLICANT: Nielsen, Peter E.
   APPLICANT: Berg, Rolf
   TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
   FILE REFERENCE: ISIS1108
   CURRENT APPLICATION NUMBER: US/08/088,661F
   CURRENT FILING DATE: 1993-07-02
   PRIOR APPLICATION NUMBER: 08/054,363
   PRIOR FILING DATE: 1993-04-26
   PRIOR APPLICATION NUMBER: PCT/EP92/01219
   PRIOR FILING DATE: 1992-05-19
   NUMBER OF SEQ ID NOS: 42
   SOFTWARE: PatentIn Ver. 2.1
   SEQ ID NO 9
   LENGTH: 16
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: Description of Artificial Sequence: No. 6228982e1 Sequence
US-08-088-661F-9

Qy      715 CTTTTTTTTTTTGATC 730
            ||||||||||||| |||
Db       16 CTTTTTTTTTTGGATC 1

Query Match       1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity   93.8%;  Pred. No. 4.3;
Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

RESULT 12
US-08-150-156A-21/c
Sequence 21, Application US/08150156A
Patent No. 6357163
GENERAL INFORMATION:
   APPLICANT:
   TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
   TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
```

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;     NUMBER OF SEQUENCES: 40
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: Wordperfect 5.1
;     CURRENT APPLICATION NUMBER: US/08/150,156A
;        APPLICATION NUMBER:
;        FILING DATE:
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: DK 0986/91
;        FILING DATE: 24-MAY-1991
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: DK 0987/91
;        FILING DATE: 24-MAY-1991
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER: DK 0510/92
;        FILING DATE: 15-APR-1992
;  INFORMATION FOR SEQ ID NO: 21:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 16 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;     PUBLICATION INFORMATION:
;        DOCUMENT NUMBER: WO PCT/EP92/01220
;        FILING DATE: 22-MAY-1992
US-08-150-156A-21

Query Match       1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity   93.8%;  Pred. No. 4.3;
Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      715 CTTTTTTTTTTTGATC 730
            ||||||||||||| |||
Db       16 CTTTTTTTTTTGGATC 1

RESULT 13
US-08-108-591B-1/c
Sequence 1, Application US/08108591B
Patent No. 6395474
GENERAL INFORMATION:
   APPLICANT: Buchardt, Ole
   APPLICANT: Egholm, Michael
   APPLICANT: Nielsen, Peter Eigil
   APPLICANT: Berg, Rolf Henrik
   TITLE OF INVENTION: Peptide Nucleic Acids
   FILE REFERENCE: ISIS0540
   CURRENT APPLICATION NUMBER: US/08/108,591B
   CURRENT FILING DATE: 2001-08-13
   NUMBER OF SEQ ID NOS: 43
   SOFTWARE: PatentIn version 3.1
   SEQ ID NO 1
   LENGTH: 16
   TYPE: DNA
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: No. 6395474e1 Sequence
US-08-108-591B-1

Query Match       1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity   93.8%;  Pred. No. 4.3;
Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      715 CTTTTTTTTTTTGATC 730
            ||||||||||||| |||
Db       16 CTTTTTTTTTTGGATC 1
```

Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    459 ACTTTTTTTTCTTTTT 474
          ||||||| |||||||
Db      1 ACTTTTTTTTTTTTTT 16
```

RESULT 8
US-08-689-856-6
; Sequence 6, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
;   APPLICANT: Sergei M. Gryaznov
;   TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
;   TITLE OF INVENTION: Connected Macromolecular Structures
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooley Godward LLP
;   STREET: Five Palo Alto Square, 3000 El Camino Real
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94306-2155
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/689,856
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/455,627
;   FILING DATE: 31-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Nakamura, Jackie N.
;   REGISTRATION NUMBER: 35,966
;   REFERENCE/DOCKET NUMBER: LYNX-003/01 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-843-5000
;   TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
US-08-689-856-6

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    459 ACTTTTTTTTTCTTTTT 474
          ||||||| ||||||
Db      1 ACTTTTTTTTTTTTTT 16
```

RESULT 9
US-08-471-907A-34/c
; Sequence 34, Application US/0847907A
; Patent No. 5986053
; GENERAL INFORMATION:
;   APPLICANT: Ecker, David J.
;   APPLICANT: Buchardt, Ole
;   APPLICANT: Egholm, Michael
;   APPLICANT: Nielsen, Peter E.
;   APPLICANT: Berg, Rolf H.
;   APPLICANT: M legaard, Niels E.
;   TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
;   TITLE OF INVENTION: NUCLEIC ACIDS

;   NUMBER OF SEQUENCES: 56
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: U.S.A.
;   ZIP: 19103
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/471,907A
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/088,658
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lucci, Joseph
;   REGISTRATION NUMBER: 33,307
;   REFERENCE/DOCKET NUMBER: ISIS-1052
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-568-3100
;   TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 16
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-471-907A-34

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    715 CTTTTTTTTTTTGATC 730
          |||||||||| ||||
Db     16 CTTTTTTTTTTGGATC 1
```

RESULT 10
US-09-070-477-6
; Sequence 6, Application US/09070477
; Patent No. 6048974
; GENERAL INFORMATION:
;   APPLICANT: Sergei M. Gryaznov
;   TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
;   TITLE OF INVENTION: and therapeutic applications
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
;   STREET: 465 Lincoln Centre Drive
;   CITY: Foster City
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94404
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 5.25 inch diskette
;   COMPUTER: IBM compatible
;   OPERATING SYSTEM: Windows 3.1/DOS 5.0
;   SOFTWARE: Microsoft Word for Windows, vers. 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/070,477
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/713,685
;   FILING DATE:
;   APPLICATION NUMBER: 08/461,271

; APPLICANT: M llegaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 564162srls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/088,658
; FILING DATE: 19930702
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,363
; FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-088-658-34

Qy   715 CTTTTTTTTTTTGATC 730
Db   16 CTTTTTTTTTTTGATC 1

RESULT 6
US-08-461-271-6
; Sequence 6, Application US/08461271
; Patent No. 5741643
; GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,271
; FILING DATE:
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Query Match   1.9%;   Score 14.4;   DB 1;   Length 16;
Best Local Similarity   93.8%;   Pred. No. 4.3;
Matches 15; Conservative   0; Mismatches   1;   Indels   0;   Gaps   0;

; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7794
; TELEFAX: (415) 358-7855
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-271-6

Qy   459 ACTTTTTTTTTCTTTTT 474
Db   1 ACTTTTTTTTTTTTTTT 16

RESULT 7
US-08-713-685A-6
; Sequence 6, Application US/08713685A
; Patent No. 5817795
; GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
NUMBER OF SEQUENCES: 6
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685A
; FILING DATE:
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7794
; TELEFAX: (415) 358-7855
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-713-685A-6

Query Match   1.9%;   Score 14.4;   DB 1;   Length 16;
Best Local Similarity   93.8%;

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/455,627
;   FILING DATE: 31-MAY-1995
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Nakamura, Jackie N.
;   REGISTRATION NUMBER: 35,966
;   REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-843-5000
;   TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA

US-08-455-627-6

Qy   459 ACTTTTTTTTTTCTTTTT 474
Db   1 ACTTTTTTTTTTTTTTTT 16

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 3
US-08-283-591-16/c
Sequence 16, Application US/08283591
Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND
; TITLE OF INVENTION: OLIGO -LACTAMAMIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
;   ADDRESSEE: No. 562915zris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: U.S.A.
;   ZIP: 19103
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/283,591
;   FILING DATE:
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME:
;   REGISTRATION NUMBER:
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-568-3100
;   TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 16
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

US-08-283-591-16

Qy   715 CTTTTTTTTTTTGATC 730
Db   16 CTTTTTTTTTTGGATC 1

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 4
US-08-283-591-25/c
Sequence 25, Application US/08283591
Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND
; TITLE OF INVENTION: OLIGO -LACTAMAMIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
;   ADDRESSEE: No. 562915zris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: U.S.A.
;   ZIP: 19103
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/283,591
;   FILING DATE: N/A
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME:
;   REGISTRATION NUMBER:
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-568-3100
;   TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 16
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown

US-08-283-591-25

Qy   715 CTTTTTTTTTTTGATC 730
Db   16 CTTTTTTTTTTGGATC 1

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 5
US-08-088-658-34/c
Sequence 34, Application US/08088658
Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.

```
OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.6
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Run on:        March 31, 2004, 14:10:54 ; Search time 0.001 Seconds
                                           (without alignments)
                                           358.428 Million cell updates/sec

Title:         us09477082Z
Perfect score: 753
Sequence:      1 aattagaccgcgtattgaaa.............tacactggtttttaacctt 753

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 0.5

Searched:      15 seqs, 238 residues

Total number of hits satisfying chosen parameters:     30

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 50 summaries

Database :    2rni.db:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.4	1.9	16	1	US-08-087-387-6	Sequence 6, Appl
2	14.4	1.9	16	1	US-08-455-627-6	Sequence 6, Appl
3	14.4	1.9	16	1	US-08-283-591-16	Sequence 16, Appl
4	14.4	1.9	16	1	US-08-283-591-25	Sequence 25, Appl
5	14.4	1.9	16	1	US-08-088-658-34	Sequence 34, Appl
6	14.4	1.9	16	1	US-08-461-271-6	Sequence 6, Appl
7	14.4	1.9	16	1	US-08-713-685A-6	Sequence 6, Appl
8	14.4	1.9	16	1	US-08-461-585A-6	Sequence 6, Appl
9	14.4	1.9	16	1	US-08-689-856-6	Sequence 6, Appl
10	14.4	1.9	16	1	US-08-471-907A-34	Sequence 34, Appl
11	14.4	1.9	16	1	US-08-070-477-6	Sequence 6, Appl
12	14.4	1.9	16	1	US-08-088-661F-9	Sequence 9, Appl
13	14.4	1.9	16	1	US-08-150-156A-21	Sequence 21, Appl
14	14.4	1.9	16	1	US-08-108-591B-1	Sequence 1, Appl
15	14	1.9	15	1	US-08-832-021-28	Sequence 28, Appl
16	9.8	1.3	16	1	US-08-275-951-31	Sequence 31, Appl
17	9.8	1.3	16	1	US-08-283-591-16	Sequence 16, Appl
18	9.8	1.3	16	1	US-08-283-591-25	Sequence 25, Appl
19	9.8	1.3	16	1	US-08-088-658-34	Sequence 34, Appl
20	9.8	1.3	16	1	US-08-471-907A-34	Sequence 34, Appl
21	9.8	1.3	16	1	US-08-088-661F-9	Sequence 9, Appl
22	9.8	1.3	16	1	US-08-150-156A-21	Sequence 21, Appl
23	9.8	1.3	16	1	US-08-108-591B-1	Sequence 1, Appl
24	9.4	1.2	16	1	US-08-087-387-6	Sequence 6, Appl
25	9.4	1.2	16	1	US-08-455-627-6	Sequence 6, Appl
26	9.4	1.2	16	1	US-08-461-271-6	Sequence 6, Appl
27	9.4	1.2	16	1	US-08-711-685A-6	Sequence 6, Appl
28	8.8	1.2	16	1	US-08-689-856-6	Sequence 6, Appl
29	8.8	1.2	15	1	US-09-070-477-6	Sequence 6, Appl
30	8.4	1.1	15	1	US-08-275-951-31	Sequence 31, Appl
	8.4	1.1	15	1	US-08-832-021-28	Sequence 28, Appl

ALIGNMENTS

```
RESULT 1
US-08-087-387-6
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
;   APPLICANT: Sergei M. Gryaznov
;   TITLE OF INVENTION: Oligonucleotide clamps having diagnostic andtherapeutic applic
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
;     STREET: 465 Lincoln Centre Drive
;     CITY: Foster City
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 5.25 inch diskette
;     COMPUTER: IBM compatible
;     OPERATING SYSTEM: Windows 3.1/DOS 5.0
;     SOFTWARE: Microsoft Word for Windows, vers. 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/087,387
;     FILING DATE: 19930702
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Stephen C. Macevicz
;     REGISTRATION NUMBER: 30,285
;     REFERENCE/DOCKET NUMBER: 104
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 358-7855
;     TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 16 nucleotides
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-087-387-6

  Query Match       1.9%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.3;
  Matches   15;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      459 ACTTTTTTTTCTTTTT 474
            |||||||||| |||||
Db        1 ACTTTTTTTTTTTTTT 16


RESULT 2
US-08-455-627-6
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
;   APPLICANT: Sergei M. Gryaznov
;   TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
;   TITLE OF INVENTION: Connected Macromolecular Structures
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Cooley Godward LLP
;     STREET: Five Palo Alto Square, 3000 El Camino Real
;     CITY: Palo Alto
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94306-2155
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 10
ADE43355/c
AC   ADE43355;
XX
ID   ADE43355 standard; DNA; 20 BP.
XX

XX
DT   31-OCT-2000 (first entry)
XX
DE   Antisense primer for untreated CASP8 wild type DNA.
XX
KW   CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
KW   tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
KW   death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO200039347-A1.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999; 99WO-US031280.
XX
PR   31-DEC-1998; 98US-0114308P.
XX
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Kidd VJ, Lahti JM, Teitz T;
XX
DR   WPI; 2000-452423/39.
XX
PT   Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or
PT   prognosing cancer, comprises detecting a modification of genomic DNA
PT   comprising the CASP8 gene that results in inactivation of the gene.
XX
PS   Example 3; Page 61; 107pp; English.

CC   Investigation of silencing of caspase-8 (CASP8) gene by methylation was
CC   analyzed using methylation-sensitive PCR analysis. Amplification of the
CC   5' untranslated region (UTR) of the CASP8 gene was performed in reaction
CC   mixtures containing bisulfite treated DNA. Primers AAA51818-23 were
CC   designed to produce a 320 bp fragment in the upstream region of CASP8
CC   gene extending from nucleotides +221 to +541. Wild type primers were used
CC   to amplify the corresponding region of untreated genomic DNA. Controls
CC   without DNA were also performed. CASP8, a cysteine protease, is part of
CC   the death inducing signaling complex (DISC) associated with the Fas
CC   receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
CC   suppressor gene. The CASP8 promoter region sequences, in particular
CC   Region 1 and Region 2, are crucial in the design and execution of the
CC   genomic methylation PCR analysis of CASP8 gene inactivation. Methylation
CC   PCR can be used to examine even minute amounts of patient material to
CC   demonstrate whether the CASP8 gene expresses an mRNA and protein product.
CC   The CASP8 gene has been localized to human chromosome 2q33-34. The
CC   methods are used to diagnose or prognose cancer. Cancer is treated by
CC   administering a vector that expresses a gene encoding functional CASP8 in
CC   cells. The cancer that is diagnosed or treated is a tumour in which a myc
CC   gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,
CC   juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
CC   cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
CC   can be diagnosed with the new method. A kit for screening for a compound
CC   that induces death-receptor-mediated apoptosis in cells containing an
CC   inactivated CASP8 gene is also provided.
XX
SQ   Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match   1.2%; Score 9.2; DB 1; Length 21;
Best Local Similarity   78.6%;
Matches   11; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy        670 ATGTGGAATTCGCGG 683
              ||||| ||||||||
Db          6 ATCTGCATTCGAGG 19
```

XX
DT   29-JAN-2004 (first entry)
XX
DE   Human uPA primer, SEQ ID 524.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   08-NOV-2001; 2001US-0339529P.
PR   08-NOV-2001; 2001US-0338010P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO-) GEN HOSPITAL CORP.
XX
PI   Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI   Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Example 4; Page 313; 848pp; English.

CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (urokinase plasminogen activator); SNCG (gamma-synuclein); IDE (insulin-
CC   degrading enzyme); KNSL1 (kinesin-like protein 1), LIPA (lysosomal acid
CC   lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC   presence of at least one of the allelic variant of one or more
CC   polymorphic regions is indicative of a predisposition for or the
CC   occurrence of neurodegenerative disease. The genes are all located on
CC   chromosome 10. M1 is useful for determining a predisposition for or the
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease. The present sequence is a PCR primer, which was used
CC   in the method of the invention.
XX
SQ   Sequence 20 BP; 1 A; 12 C; 2 G; 5 T; 0 U; 0 Other;

Query Match   1.1%; Score 8.6; DB 1; Length 20;
Best Local Similarity   73.3%;
Matches   11; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

```
Qy        208 ACAGGGGCTGTGCGGG 222
              ||| ||| ||||||
Db         19 AGAGGGCAGGGAGG 5
```

Search completed: March 31, 2004, 14:10:08
Job time : 0.001 secs

CC   PCR can be used to examine even minute amounts of patient material to
CC   demonstrate whether the CASP8 gene expresses an mRNA and protein product.
CC   The CASP8 gene has been localized to human chromosome 2q33-34. The
CC   methods are used to diagnose or prognose cancer. Cancer is treated by
CC   administering a vector that expresses a gene encoding functional CASP8 in
CC   cells. The cancer that is diagnosed or treated is a tumour in which a myc
CC   gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,
CC   juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
CC   cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
CC   can be diagnosed with the new method. A kit for screening for a compound
CC   that induces death-receptor-mediated apoptosis in cells containing an
CC   inactivated CASP8 gene is also provided
XX
SQ   Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match   1.5%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   340 GCAGTCTCCAGTTCCTCT 357
         ||||||||| |||| |||
Db   19 GCAGTCTCCGAGTCCCT 2

RESULT 7
AAQ20008/c
ID   AAQ20008 standard; DNA; 16 BP.
XX
AC   AAQ20008;
XX
DT   01-APR-1992 (first entry)
XX
DE   Oligonucleotide #4 able to covalently cross-link to target DNA.
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   modified_base 8
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "N4N4-ethanocytosine"
FT   modified_base 14
FT   /*tag= b
FT   /mod_base= m5c
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990; 90US-00529346.
XX
PR   25-MAY-1990; 90US-00529346.
PR   14-JAN-1991; 91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD, Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
Example 2: Page 21; 42pp; English.

The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
one of four oligonucleotides which were designed to specifically bind and
cross-link to the duplex target sequence AAQ20004. Oligo #4 with its
internal cross-linking group was less effective than the other

CC   oligonucleotides with terminal cross-linking groups. See also AAQ20005-7
XX
SQ   Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

Query Match   1.4%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   19 AAGTAAAAGAAA 30
         || |||||||||
Db   16 AAGAAAAAGAAA 5

RESULT 8
AAX18362/c
ID   AAX18362 standard; DNA; 16 BP.
XX
AC   AAX18362;
XX
DT   11-MAY-1999 (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 3.
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997; 97JP-00208312.
XX
PR   18-JUL-1997; 97JP-00208312.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates
to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
natural number indicating the repetition of alpha; beta, delta = V or N;
V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
thymine; gamma = thymine; k = natural number of 3 or over indicating the
repetition of gamma, in which thymine expressed by gamma is composed of
1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
useful as primers for RT-PCR and determination of base sequences. The new
sequences allow for reproductive and highly efficient analysis of gene
sequences

SQ   Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match   1.4%; Score 10.2; DB 1; Length 16;
Best Local Similarity 80.0%;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   16 TGAAAGTAAAAGAAA 30
         ||||| |||| ||
Db   16 TGAAAAAAAAAAAA 2

RESULT 9
AAA51823
ID   AAA51823 standard; DNA; 21 BP.
XX
AC   AAA51823;

FT   modified_base
FT   14
FT   /*tag= b
FT   /mod_base= m5c
XX
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PD   25-MAY-1990;
XX
PF   25-MAY-1990; 90US-00529346.
XX
PR   90US-00529346.
PR   14-JAN-1991; 91US-00640054.
XX
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD, Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 2; Page 21; 42pp; English.
XX
CC   The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
CC   one of four oligonucleotides which were designed to specifically bind and
CC   cross-link to the duplex target sequence AAQ20004. Oligo #4 with its
CC   internal cross-linking group was less effective than the other
CC   oligonucleotides with terminal cross-linking groups. See also AAQ20005-7
XX
SQ   Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

Qy   462 TTTTTTTTTCTTTTTCAT 477
          ||||||||||||||||
Db   1 TTTTTTTTTCTTTTTTCTT 16

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.7;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 5
AAX18362
ID   AAX18362 standard; DNA; 16 BP.
XX
AC   AAX18362;
XX
DT   11-MAY-1999 (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 3.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP1032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997; 97JP-00208312.
XX
PR   18-JUL-1997; 97JP-00208312.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.

CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha]n-beta
CC   -N3'/or (X)m5'-(gamma]k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine or
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Qy   461 TTTTTTTTTCTTTTTCA 476
          |||||||||| ||||||
Db   1 TTTTTTTTTTTTTTTTCA 16

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.7;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 6
AAA51822/c
ID   AAA51822 standard; DNA; 21 BP.
XX
AC   AAA51822;
XX
DT   31-OCT-2000 (first entry)
XX
DE   Sense primer for untreated CASP8 wild type DNA.
XX
KW   CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
KW   tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
KW   death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039347-A1.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999; 99WO-US031280.
XX
PR   31-DEC-1998; 98US-0114308P.
XX
PA   (SJUD-) ST JUDE CHILDREN S RES HOSPITAL.
XX
PI   Kidd VJ, Lahti JM, Teitz T;
XX
DR   WPI; 2000-452423/39.
XX
PT   Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or
PT   prognosing cancer, comprises detecting a modification of genomic DNA
PT   comprising the CASP8 gene that results in inactivation of the gene.
XX
PS   Example 3; Page 61; 107pp; English.
XX
CC   Investigation of silencing of caspase-8 (CASP8) gene by methylation was
CC   analyzed using methylation-sensitive PCR analysis. Amplification of the
CC   5' untranslated region (UTR) of the Casp8 gene was performed in reaction
CC   mixtures containing bisulfite treated DNA. Primers AAA51818-23 were
CC   designed to produce a 320 bp fragment in the upstream region of Casp8
CC   gene extending from nucleotides +221 to +541. Wild type primers were used
CC   to amplify the corresponding region of untreated genomic DNA. Controls
CC   without DNA were also performed. CASP8, a cysteine protease, is part of
CC   the death inducing signaling complex (DISC) associated with the Fas
CC   receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
CC   suppressor gene. The CASP8 promoter region sequences, in particular
CC   Region 1 and Region 2, are crucial to the design and execution of the
CC   genomic methylation PCR analysis of CASP8 gene inactivation. Methylation

```
PD   06-JUL-2000.
XX
PF   30-DEC-1999;  99WO-US031280.
XX
PR   31-DEC-1998;  98US-0114308P.
XX
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Kidd VJ, Lahti JM, Teitz T;
XX
DR   WPI; 2000-452423/39.
XX
PT   Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or
PT   prognosing cancer, comprises detecting a modification of genomic DNA
PT   comprising the CASP8 gene that results in inactivation of the gene.
XX
PS   Example 3; Page 61; 107pp; English.
XX
CC   Investigation of silencing of caspase-8 (CASP8) gene by methylation was
CC   analyzed using methylation-sensitive PCR analysis. Amplification of the
CC   5' untranslated region (UTR) of the Casp8 gene was performed in reaction
CC   mixtures containing bisulfite treated DNA. Primers AAA51818-23 were
CC   designed to produce a 320 bp fragment in the upstream region of Casp8
CC   gene extending from nucleotides +221 to +541. Wild type primers were used
CC   to amplify the corresponding region of untreated genomic DNA. Controls
CC   without DNA were also performed. CASP8, a cysteine protease, is part of
CC   the death inducing signaling complex (DISC) associated with the Fas
CC   receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
CC   suppressor gene. The CASP8 promoter region sequences, in particular
CC   Region 1 and Region 2, are crucial to the design and execution of the
CC   genomic methylation PCR analysis of CASP8 gene inactivation. Methylation
CC   PCR can be used to examine even minute amounts of patient material to
CC   demonstrate whether the CASP8 gene expresses an mRNA and protein product.
CC   The CASP8 gene has been localized to human chromosome 2q33-34. The
CC   methods are used to diagnose or prognose cancer. Cancer is treated by
CC   administering a vector that expresses a gene encoding functional CASP8 in
CC   cells. The cancer that is diagnosed or treated is a tumour in which a myc
CC   gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,
CC   juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
CC   cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
CC   can be diagnosed with the new method. A kit for screening for a compound
CC   that induces death-receptor-mediated apoptosis in cells containing an
CC   inactivated CASP8 gene is also provided
XX
SQ   Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match             2.8%;  Score 21;  DB 1;  Length 21;
Best Local Similarity   100.0%;
Matches   21;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    388  CGCCTTCGGAATGCAGATACACG  408
           |||||||||||||||||||||||
Db     21  CGCCTTCGGAATGCAGATACACG  1


RESULT 3
ADE43355
ID   ADE43355 standard; DNA; 20 BP.
XX
AC   ADE43355;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human uPA primer, SEQ ID 524.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200305443-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002;  2002WO-US034679.
XX
PR   25-OCT-2001;  2001US-0339525P.
PR   08-NOV-2001;  2001US-0336929P.
PR   08-NOV-2001;  2001US-0338010P.
PR   09-NOV-2001;  2001US-0338363P.
PR   04-DEC-2001;  2001US-0337052P.
PR   28-MAR-2002;  2002US-0368191P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO-) GEN HOSPITAL CORP.
XX
PI   Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI   Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Example 4; Page 313; 848pp; English.
XX
CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC   degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC   lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC   presence of at least one of the allelic variant of one or more
CC   polymorphic regions is indicative of a predisposition for or the
CC   occurrence of neurodegenerative disease. The genes are all located on
CC   chromosome 10. M1 is useful for determining a predisposition for or the
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease. The present sequence is a PCR primer, which was used
CC   in the method of the invention.
XX
SQ   Sequence 20 BP; 1 A; 12 C; 2 G; 5 T; 0 U; 0 Other;

Query Match             2.4%;  Score 18;  DB 1;  Length 20;
Best Local Similarity   100.0%;
Matches   18;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    613  TCCCCTCCCTGCCCTCTG  630
           ||||||||||||||||||
Db      3  TCCCCTCCCTGCCCTCTG  20


RESULT 4
AAQ20008
ID   AAQ20008 standard; DNA; 16 BP.
XX
AC   AAQ20008;
XX
DT   01-APR-1992  (first entry)
XX
DE   Oligonucleotide #4 able to covalently cross-link to target DNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   modified_base  8
FT                  /*tag=  a
FT                  /mod_base= OTHER
FT                  /note= "N4N4-ethanocytosine"
```

OM nucleic - nucleic search, using sw model

```
                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2004 Compugen Ltd.
```

Run on: March 31, 2004, 14:10:07 ; Search time 0.001 Seconds
                        (without alignments)
                        141.564 Million cell updates/sec

Title: us09470822
Perfect score: 753
Sequence: 1 aattagaccggtattgaaa..............tacacggttctttaacctt 753

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 94 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 50 summaries

Database : 2rng.db:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                    SUMMARIES

```
                            %
Result               Query
No.  Score  Match Length DB  ID        Description
---- -----  ----- ------ --  --------   -----------
  1   21    2.8     21   1   AAA51822   Sense primer for u
  2   21    2.8     21   1   AAA51823   Antisense primer f
  3   18    2.4     20   1   ADB43355   Human uPA primer,
c 4   14.4  1.9     16   1   AAQ20008   Oligonucleotide #4
  5   14.4  1.9     16   1   AAX18362   RT-PCR primer of t
c 6   11.6  1.5     21   1   AAA51822   Sense primer for u
c 7   10.4  1.4     16   1   AAQ20008   Oligonucleotide #4
c 8   10.2  1.4     16   1   AAX18362   Antisense primer o
c 9   9.2   1.2     21   1   AAA51823   RT-PCR primer of t
c 10  8.6   1.1     20   1   ADB43355   Human uPA primer,
```

                                    ALIGNMENTS

RESULT 1
```
ID   AAA51822
AC   AAA51822;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Sense primer for untreated CASP8 wild type DNA.
XX
KW   CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
KW   tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
KW   death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039347-A1.
XX
```

AAA51822 standard; DNA; 21 BP.

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PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031280.
XX
PR   31-DEC-1998;   98US-01143308P.
XX
PA   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI   Kidd VJ, Lahti JM, Teitz T;
XX
DR   WPI; 2000-452423/39.
XX
PS   Example 3; Page 61; 107pp; English.
XX
```

```
CC   Investigation of silencing of caspase-8 (CASP8) gene by methylation was
CC   analyzed using methylation-sensitive PCR analysis. Amplification of the
CC   5' untranslated region (UTR) of the CASP8 gene was performed in reaction
CC   mixtures containing bisulfite treated DNA. Primers AAA51818-23 were
CC   designed to produce a 320 bp fragment in the upstream region of CASP8
CC   gene extending from nucleotides +221 to +541. Wild type primers were used
CC   to amplify the corresponding region of untreated genomic DNA. Controls
CC   without DNA were also performed. CASP8, a cysteine protease, is part of
CC   the death inducing signaling complex (DISC) associated with the Fas
CC   receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
CC   suppressor gene. The CASP8 promoter region sequences, in particular
CC   Region 1 and Region 2, are crucial to the design and execution of the
CC   genomic methylation PCR analysis of CASP8 gene inactivation. Methylation
CC   PCR can be used to examine even minute amounts of patient material to
CC   demonstrate whether the CASP8 gene expresses an mRNA and protein product.
CC   The CASP8 gene has been localized to human chromosome 2q33-34. The
CC   methods are used to diagnose or prognose cancer. Cancer is treated by
CC   administering a vector that expresses a gene encoding functional CASP8 in
CC   cells. The cancer that is diagnosed or treated is a tumour in which a myc
CC   gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,
CC   juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
CC   cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
CC   can be diagnosed with the new method. A kit for screening for a compound
CC   that induces death-receptor-mediated apoptosis in cells containing an
CC   inactivated CASP8 gene is also provided
XX
SQ   Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
```

```
Query Match     2.8%;  Score 21;  DB 1;  Length 21;
Best Local Similarity   100.0%;
Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy           90 TAGGGGGACTCGGAGACTGCGA 110
                |||||||||||||||||||||||
Db            1 TAGGGGGACTCGGAGACTGCGA 21
```

RESULT 2
```
ID   AAA51823
AC   AAA51823;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Antisense primer for untreated CASP8 wild type DNA.
XX
KW   CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
KW   tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
KW   death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039347-A1.
XX
```

AAA51823/c
AAA51823 standard; DNA; 21 BP.

RESULT 27
LOCUS   AR051238/c
DEFINITION AR051238
ACCESSION   Sequence 6 from patent US 5830658.
VERSION   AR051238
KEYWORDS   AR051238.1 GI:5974602
SOURCE   .
ORGANISM   Unknown.
            Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS   Gryaznov,S.M.
TITLE   Convergent synthesis of branched and multiply connected
            macromolecular structures
JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES   Location/Qualifiers
source   1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match   1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity   90.9%;   Pred. No. 27;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   643 AAAAAACAAGT 653
                |||||||| |||
Db   11 AAAAAAAAAGT 1

RESULT 28
LOCUS   I16032/c   16 bp   DNA   linear   PAT 03-APR-1996
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION   I16032.1 GI:1250940
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
TITLE   Oligonucleotide clamps having diagnostic applications
JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES   Location/Qualifiers
source   1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match   1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity   90.9%;   Pred. No. 27;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   643 AAAAAACAAGT 653
                |||||||| |||
Db   11 AAAAAAAAAGT 1

RESULT 29
LOCUS   I28367/c   16 bp   DNA   linear   PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION   I28367.1 GI:1819143
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS   Gryaznov,S.M.
TITLE   Convergent synthesis of branched and multiply connected
            macromolecular structures
JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES   Location/Qualifiers
source   1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match   1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity   90.9%;   Pred. No. 27;
Matches   10; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   643 AAAAAACAAGT 653
                |||||||| |||
Db   11 AAAAAAAAAGT 1

RESULT 30
LOCUS   AR231294/c   15 bp   DNA   linear   PAT 20-DEC-2002
DEFINITION AR231294
            Sequence 31 from patent US 6451968.
ACCESSION   AR231294
VERSION   AR231294.1 GI:27272225
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
TITLE   Peptide nucleic acids
JOURNAL   Patent: US 6451968-A 31 17-SEP-2002;
FEATURES   Location/Qualifiers
source   1..15
                     /organism="unknown"
                     /mol_type="genomic DNA"

Query Match   1.2%; Score 8.8; DB 1; Length 15;
Best Local Similarity   83.3%;   Pred. No. 31;
Matches   10; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   18 AAAGTAAAAGAA 29
                |||| ||||| ||
Db   14 AAAGAAAAAAA 3

Search completed: March 31, 2004, 14:08:57
Job time : 1 secs

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RESULT 22
LOCUS       I49619                    16 bp    DNA      linear   PAT 07-OCT-1997
DEFINITION  Sequence 34 from patent US 5641625.
ACCESSION   I49619
VERSION     I49619.1  GI:2471839
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
            Mollegaard,N.E.
  TITLE     Cleaving double-stranded DNA with peptide nucleic acids
  JOURNAL   Patent: US 5641625-A 34 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Qy        640 CCCAAAAAACAAG 652
              ||| ||||| |||
Db          4 CCAAAAAAAAAG 16

Query Match             1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;
Matches    11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;


RESULT 23
LOCUS       AR200478                  16 bp    DNA      linear   PAT 20-APR-2002
DEFINITION  Sequence 21 from patent US 6357163.
ACCESSION   AR200478
VERSION     AR200478.1  GI:20251366
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 21 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Qy        640 CCCAAAAAACAAG 652
              ||| ||||| |||
Db          4 CCAAAAAAAAAG 16


RESULT 24
LOCUS       AR371265                  16 bp    DNA      linear   PAT 12-SEP-2003
DEFINITION  Sequence 1 from patent US 6395474.
ACCESSION   AR371265
VERSION     AR371265.1  GI:34608197
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

Query Match             1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;
Matches    11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        640 CCCAAAAAACAAG 652
              ||| ||||| |||
Db          4 CCAAAAAAAAAG 16
```

```
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 1 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
                     /mol_type="genomic DNA"

Qy        640 CCCAAAAAACAAG 652
              ||| ||||| |||
Db          4 CCAAAAAAAAAG 16

Query Match             1.3%;  Score 9.8;  DB 1;  Length 16;
Best Local Similarity   84.6%;
Matches    11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;


RESULT 25
LOCUS       AR002257/c                16 bp    DNA      linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Qy        643 AAAAAACAAGT 653
              |||||| ||||
Db         11 AAAAAAAAAGT 1

Query Match             1.2%;  Score 9.4;  DB 1;  Length 16;
Best Local Similarity   90.9%;
Matches    10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


RESULT 26
LOCUS       AR045207/c                16 bp    DNA      linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Qy        643 AAAAAACAAGT 653
              |||||| ||||
Db         11 AAAAAAAAAGT 1

Query Match             1.2%;  Score 9.4;  DB 1;  Length 16;
Best Local Similarity   90.9%;
Matches    10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
             Mollegaard,N.E.
TITLE   Peptide nucleic acids complexes of two peptide nucleic acid strands
             and one nucleic acid strand
JOURNAL   Patent: US 5986053-A 34 16-NOV-1999;
FEATURES
     source   Location/Qualifiers
                      1..16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

Qy   640 CCCAAAAAAACAAG 652
                 ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

RESULT 18
LOCUS   AR150597
DEFINITION   Sequence 9 from patent US 6228982.
ACCESSION   AR150597
VERSION   AR150597.1   GI:15115188
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and
             Berg,R.
  TITLE   Double-stranded peptide nucleic acids
  JOURNAL   Patent: US 6228982-A 9 08-MAY-2001;
FEATURES   Location/Qualifiers
     source   1..16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

Query Match   1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   640 CCCAAAAAAACAAG 652
                 ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

RESULT 19
LOCUS   E36063
DEFINITION   Higher-order structure and binding of peptide nucleic acid
ACCESSION   E36063
VERSION   E36063   GI:13022465
KEYWORDS   .
SOURCE   unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
             Morugado,N.A.
  TITLE   Higher-order structure and binding of peptide nucleic acid
  JOURNAL   Patent: JP 199236396-A 8 31-AUG-1999;
             ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN
             PATER A, BERGH RORUFU HO
COMMENT   OS   Unidentified
             PN   JP 199236396-A/8
             PD   31-AUG-1999
             PF   14-OCT-1998 JP 199291590
             PR   02-JUL-1993 US 08858
             PI   BUSHATO ORB,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
             PI   EKKA DAVID JAY,MORUGADO NIIUS A
             PC   C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,

FEATURES
     source   Location/Qualifiers
                      1..16
                      /organism='Unidentified'.

Qy   640 CCCAAAAAAACAAG 652
                 ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

Query Match   1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS   AR150597   16 bp   DNA   linear   PAT 08-AUG-2001

PC   C07H21/02,
PC   C12N15/09,C12Q1/68,C12N15/00
PC   Strandedness: Single;
FH   Topology: Linear;
FT   Key
     source   Location/Qualifiers
FT   1..16
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Qy   640 CCCAAAAAAACAAG 652
                 ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

RESULT 20
LOCUS   I42181
DEFINITION   Sequence 16 from patent US 5629152.
ACCESSION   I42181
VERSION   I42181.1   GI:2467676
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Ravikumar,V.
  TITLE   Trisubstituted .beta.-lactams and oligo .beta.-lactamamides
  JOURNAL   Patent: US 5629152-A 16 13-MAY-1997;
FEATURES   Location/Qualifiers
     source   1..16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

Query Match   1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS   I42181   16 bp   DNA   linear   PAT 07-OCT-1997

Qy   640 CCCAAAAAAACAAG 652
                 ||||||||| |||
Db   4 CCAAAAAAAAAAG 16

RESULT 21
LOCUS   I42187
DEFINITION   Sequence 25 from patent US 5629152.
ACCESSION   I42187
VERSION   I42187.1   GI:2467682
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Ravikumar,V.
  TITLE   Trisubstituted .beta.-lactams and oligo .beta.-lactamamides
  JOURNAL   Patent: US 5629152-A 25 13-MAY-1997;
FEATURES   Location/Qualifiers
     source   1..16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

Query Match   1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS   I42187   16 bp   DNA   linear   PAT 07-OCT-1997

RESULT 13

```
Qy      715 CTTTTTTTTTTTGATC 730
            |||||||||||||||
Db       16 CTTTTTTTTTTTGATC 1
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```
Query Match         1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity  93.8%;  Pred. No. 4.3;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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LOCUS	AR200478	16 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 21 from patent US 6357163.
ACCESSION	AR200478
VERSION	AR200478.1 GI:20251366
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 16)
AUTHORS	Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE	Use of nucleic acid analogues in diagnostics and analytical
	procedures
JOURNAL	Patent: US 6357163-A 21 19-MAR-2002;
FEATURES	Location/Qualifiers
source	1..16
	/organism="unknown"
	/mol_type="unassigned DNA"

RESULT 14

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Qy      715 CTTTTTTTTTTTGATC 730
            |||||||||||||||
Db       16 CTTTTTTTTTTTGATC 1
```

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Query Match         1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity  93.8%;  Pred. No. 4.3;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
```

LOCUS	AR371265/c	16 bp	DNA	linear	PAT 12-SEP-2003
DEFINITION	Sequence 1 from patent US 6395474.
ACCESSION	AR371265
VERSION	AR371265.1 GI:34608197
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 16)
AUTHORS	Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE	Peptide nucleic acids
JOURNAL	Patent: US 6395474-A 1 28-MAY-2002;
FEATURES	Location/Qualifiers
source	1..16
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	/mol_type="genomic DNA"

RESULT 15

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Db       16 CTTTTTTTTTTTGGATC 1
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Query Match         1.9%;  Score 14.4;  DB 1;  Length 16;
Best Local Similarity  93.8%;  Pred. No. 4.3;
Matches  15;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
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LOCUS	AR231294	15 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 31 from patent US 6451968.
ACCESSION	AR231294
VERSION	AR231294.1 GI:27272225
REFERENCE	

KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
	Coull,J.M., Kiely,J. and Griffith,M.
TITLE	Peptide nucleic acids
JOURNAL	Patent: US 6451968-A 31 17-SEP-2002;
FEATURES	Location/Qualifiers
source	1..15
	/organism="unknown"
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Qy      460 CTTTTTTTTTCTTTT 473
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Best Local Similarity  100.0%;  Pred. No. 5.6;
Matches  14;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 16

LOCUS	A36563	16 bp	DNA	linear	PAT 05-MAR-1997
DEFINITION	Sequence 3 from Patent WO9325706.
ACCESSION	A36563
VERSION	A36563.1 GI:2293876
KEYWORDS	.
SOURCE	unidentified
ORGANISM	unidentified
	unclassified.
REFERENCE	1 (bases 1 to 16)
AUTHORS	Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Stanley,C.J.
TITLE	USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF NUCLEIC ACID
	AMPLIFICATION
JOURNAL	Patent: WO 9325706-A 3 23-DEC-1993;
	BUCHARDT OLE (DK)
COMMENT	Other publication CZ 9402951 950913
	Other publication AU 4323593 940104
	Other publication CA 2136831 931223
	Other publication SK 149394 960110
	Other publication HU 71931 960228
	Other publication FI 945725 941205
	Other publication NO 944655 950203
	Other publication JP 8501681T 960227.
FEATURES	Location/Qualifiers
source	1..16
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RESULT 17

LOCUS	AR087164	16 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 34 from patent US 5986053.
ACCESSION	AR087164
VERSION	AR087164.1 GI:10013927
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 16)

RESULT 8
LOCUS   I16032   16 bp   DNA   linear   PAT 03-APR-1996
DEFINITION   Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION   I16032.1 GI:1250940
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE   Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES   Location/Qualifiers
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Best Local Similarity   93.8%;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 9
LOCUS   I28367   16 bp   DNA   linear   PAT 06-FEB-1997
DEFINITION   Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION   I28367.1 GI:1819143
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE   Convergent synthesis of branched and multiply connected
                macromolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"

Qy   459 ACTTTTTTTTTTCTTTT 474
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Db   1 ACTTTTTTTTTTTTTTT 16

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 10
LOCUS   I42181   16 bp   DNA   linear   PAT 07-OCT-1997
DEFINITION   Sequence 16 from patent US 5629152.
ACCESSION   I42181
VERSION   I42181.1 GI:2467676
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Ravikumar,V.
  TITLE   Trisubstituted .beta.-lactams and oligo .beta.-lactamamides
  JOURNAL   Patent: US 5629152-A 16 13-MAY-1997;
FEATURES   Location/Qualifiers
     source   1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

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Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 11
LOCUS   I42187   16 bp   DNA   linear   PAT 07-OCT-1997
DEFINITION   Sequence 25 from patent US 5629152.
ACCESSION   I42187
VERSION   I42187.1 GI:2467682
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Ravikumar,V.
  TITLE   Trisubstituted .beta.-lactams and oligo .beta.-lactamamides
  JOURNAL   Patent: US 5629152-A 25 13-MAY-1997;
FEATURES   Location/Qualifiers
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Db   16 CTTTTTTTTTTTTGGATC 1

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Best Local Similarity   93.8%;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 12
LOCUS   I49619   16 bp   DNA   linear   PAT 07-OCT-1997
DEFINITION   Sequence 34 from patent US 5641625.
ACCESSION   I49619
VERSION   I49619.1 GI:2471839
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
                Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
                Mollegaard,N.E.
  TITLE   Cleaving double-stranded DNA with peptide nucleic acids
  JOURNAL   Patent: US 5641625-A 34 24-JUN-1997;
FEATURES   Location/Qualifiers
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Query Match   1.9%; Score 14.4; DB 1; Length 16;
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VERSION     AR045207.1  GI:5966672
KEYWORDS    Unknown.
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
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Qy      459 ACTTTTTTTTTTCTTTTT 474
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Db        1 ACTTTTTTTTTTTTTTTT 16
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Query Match             1.9%;  Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%;        Pred. No. 4.3;
Matches  15;  Conservative   0; Mismatches   1; Indels   0; Gaps   0;
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RESULT 4
LOCUS       AR051238               16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="unknown"
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Qy      459 ACTTTTTTTTTTCTTTTT 474
            ||||||||||| ||||||
Db        1 ACTTTTTTTTTTTTTTTT 16
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RESULT 5
LOCUS       AR087164               16 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 34 from patent US 5986053.
ACCESSION   AR087164
VERSION     AR087164.1  GI:10013927
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
            Mollegaard,N.E.
  TITLE     Peptide nucleic acids complexes of two peptide nucleic acid strands
            and one nucleic acid strand
  JOURNAL   Patent: US 5986053-A 34 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1..16
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Query Match             1.9%;  Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%;        Pred. No. 4.3;
Matches  15;  Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy      715 CTTTTTTTTTTTGATC 730
            |||||||||||| |||
Db       16 CTTTTTTTTTTTGGATC 1
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RESULT 6
LOCUS       AR150597               16 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6228982.
ACCESSION   AR150597
VERSION     AR150597.1  GI:15115188
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and
            Berg,R.
  TITLE     Double-stranded peptide nucleic acids
  JOURNAL   Patent: US 6228982-A 9 08-MAY-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"

Qy      715 CTTTTTTTTTTTGATC 730
            |||||||||||| |||
Db       16 CTTTTTTTTTTTGGATC 1
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Query Match             1.9%;  Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%;        Pred. No. 4.3;
Matches  15;  Conservative   0; Mismatches   1; Indels   0; Gaps   0;
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```
RESULT 7
LOCUS       E36063                 16 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Higher-order structure and binding of peptide nucleic acid.
ACCESSION   E36063
VERSION     E36063.1  GI:13022465
KEYWORDS
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
            Morugado,N.A.
  TITLE     Higher-order structure and binding of peptide nucleic acid
  JOURNAL   Patent: JP 1999236396-A 8 31-AUG-1999;
            ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN
            PATER A, BERGH RORUFU HO
COMMENT     OS   Unidentified
            PN   JP 1999236396-A/8
            PD   31-AUG-1999
            PF   14-OCT-1998 JP 1998291590
            PR   02-JUL-1993 US     088658
            PI   BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
            PI   EKKA DAVID JAY,MORUGADO NIIUS A
            PC   C07H21/04,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
            PC   C07H21/02,C12Q1/68,C12N15/00
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            PC   Key                 Location/Qualifiers
            FH
            FT   source              1..16
                                     /organism='Unidentified',
FEATURES             Location/Qualifiers
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: March 31, 2004, 14:08:56 ; Search time 0.001 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 15 seqs, 239 residues

Total number of hits satisfying chosen parameters: 30

Minimum Match 0%
Maximum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 50 summaries

Database :   2rge.db:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match	DB	ID	Description
1	14.4	1.9	16	1	A36563	ACCESSION:A36563
2	14.4	1.9	16	1	AR002257	ACCESSION:AR002257
3	14.4	1.9	16	1	AR045207	ACCESSION:AR045207
4	14.4	1.9	16	1	AR051238	ACCESSION:AR051238
5	14.4	1.9	16	1	AR087164	ACCESSION:AR087164
6	14.4	1.9	16	1	AR150597	ACCESSION:AR150597
7	14.4	1.9	16	1	E36063	ACCESSION:E36063
8	14.4	1.9	16	1	I16032	ACCESSION:I16032
9	14.4	1.9	16	1	I28367	ACCESSION:I28367
10	14.4	1.9	16	1	I42181	ACCESSION:I42181
11	14.4	1.9	16	1	I42187	ACCESSION:I42187
12	14.4	1.9	16	1	I49619	ACCESSION:I49619
13	14.4	1.9	16	1	AR200478	ACCESSION:AR200478
14	14.4	1.9	16	1	AR371265	ACCESSION:AR371265
15	14	1.9	15	1	AR231294	ACCESSION:AR231294
16	9.8	1.9	16	1	A36563	ACCESSION:A36563
17	9.8	1.9	16	1	AR087164	ACCESSION:AR087164
18	9.8	1.9	16	1	AR150597	ACCESSION:AR150597
19	9.8	1.3	16	1	E36063	ACCESSION:E36063
20	9.8	1.3	16	1	I42181	ACCESSION:I42181
21	9.8	1.3	16	1	I42187	ACCESSION:I42187
22	9.8	1.3	16	1	I49619	ACCESSION:I49619
23	9.8	1.3	16	1	AR200478	ACCESSION:AR200478
24	9.8	1.3	16	1	AR371265	ACCESSION:AR371265
25	9.4	1.2	16	1	AR002257	ACCESSION:AR002257
26	9.4	1.2	16	1	AR045207	ACCESSION:AR045207
27	9.4	1.2	16	1	AR051238	ACCESSION:AR051238
28	9.4	1.2	16	1	I16032	ACCESSION:I16032
29	9.4	1.2	16	1	I28367	ACCESSION:I28367
30	8.8	1.2	15	1	AR231294	ACCESSION:AR231294

ALIGNMENTS

RESULT 1
LOCUS   A36563   16 bp   DNA   linear   PAT 05-MAR-1997
DEFINITION   A36563 Sequence 3 from Patent WO9325706.
ACCESSION   A36563
VERSION   A36563.1 GI:2293876
KEYWORDS   .
SOURCE   unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Stanley,C.J.
  TITLE   USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF NUCLEIC ACID
             AMPLIFICATION
  JOURNAL   Patent: WO 9325706-A 3 23-DEC-1993;
             BUCHARDT OLE (DK)
COMMENT   Other publication CZ 9902951 950913
             Other publication AU 4323593 940104
             Other publication CA 2136831 931223
             Other publication SK 149394 960110
             Other publication HU 71931 960228
             Other publication PI 94725 941205
             Other publication NO 944655 950203
             Other publication JP 85016811 960227.
FEATURES   Location/Qualifiers
     source   1..16
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
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Qy   715 CTTTTTTTTTTTGATC 730
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Db   16 CTTTTTTTTTTGGATC 1

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 2
LOCUS   AR002257   16 bp   DNA   linear   PAT 04-DEC-1998
DEFINITION   Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION   AR002257.1 GI:3963811
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE   Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES   Location/Qualifiers
     source   1..16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Qy   459 ACTTTTTTTTTCTTTTT 474
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Db   1 ACTTTTTTTTTTTTTTT 16

Query Match   1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity   93.8%; Pred. No. 4.3;
Matches   15; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

RESULT 3
LOCUS   AR045207   16 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION   Sequence 6 from patent US 5817795.

PT   respectively, for targetting sequences on alternate strands of DHNA to
PT   control gene expression.
XX
PS   Example 2; Fig 4B; 108pp; English.
XX
CC   The present invention relates to methods and oligonucleotides for forming
CC   a triple-helix comprising a double helical nucleic acid comprising first
CC   and second substantially complementary strands, and an oligonucleotide
CC   bound to a purine-rich target sequence within the double helical nucleic
CC   acid, where the oligonucleotide binds in a parallel and antiparallel
CC   orientation, respectively, to target sequences on alternate strands of
CC   the double helical nucleic acid. The method has therapeutic applications,
CC   where gene expression is controlled by selective triple-helix formation
CC   within expression regulatory sequences of a target gene. The
CC   oligonucleotides can be used to form triple-helices, and are useful to
CC   detect the presence or absence of specific sequences within genomic DNA
CC   for diagnostic and therapeutic purposes. The oligonucleotides can be
CC   selected to specifically bind to pathogenic double-stranded DNA including
CC   specific sequences required by pathogenic bacteria or viruses for
CC   replication or virulence, reducing their pathogenicity. Alternatively,
CC   the oligonucleotide can be chosen to target a unique sequence of the
CC   pathogen which is not found in the genome of pathogen's host. The
CC   oligonucleotides can be used in cancer treatment by way of triple-helix
CC   suppression of specific oncogenes including those of endogenous or viral
CC   origin. Such therapeutic oligonucleotides are capable of forming triple-
CC   helices with such sequences in cancerous cells containing the activated
CC   oncogene, so preferentially killing or repressing the cancer causing
CC   cell. The present sequence represents an oligonucleotide used in the
CC   methods of the present invention
XX
SQ   Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

     Query Match   1.2%;   Score 8.2;   DB 1;   Length 15;
     Best Local Similarity   76.9%;   Pred. No. 0;
     Matches   10;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;

Qy   255 AGGCAAAGGGAAA 267
              || |||| |||
Db   15 AGAGAAAGAGAAA 3

Search completed: March 31, 2004, 14:06:04
Job time : 0.001 secs

DR   WPI; 2002-536030/57.
XX
XX
PT   A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT   oligonucleotide which binds in parallel and antiparallel orientation,
PT   respectively, for targeting sequences on alternate strands of DHNA to
PT   control gene expression.
XX
PS   Example 2; Fig 4B; 108pp; English.
XX
CC   The present invention relates to methods and oligonucleotides for forming
CC   a triple-helix comprising a double helical nucleic acid comprising first
CC   and second substantially complementary strands, and an oligonucleotide
CC   bound to a purine-rich target sequence within the double helical nucleic
CC   acid, where the oligonucleotide binds in a parallel and antiparallel
CC   orientation, respectively, to target sequences on alternate strands of
CC   the double helical nucleic acid. The method has therapeutic applications,
CC   where gene expression is controlled by selective triple-helix formation
CC   within expression regulatory sequences of a target gene. The
CC   oligonucleotides can be used to form triple-helices, and are useful to
CC   detect the presence or absence of specific sequences within genomic DNA
CC   for diagnostic and therapeutic purposes. The oligonucleotides can be
CC   selected to specifically bind to pathogenic double-stranded DNA including
CC   specific sequences required by pathogenic bacteria or viruses for
CC   replication or virulence, reducing their pathogenicity. Alternatively,
CC   the oligonucleotide can be chosen to target a unique sequence of the
CC   pathogen which is not found in the genome of pathogen's host. The
CC   oligonucleotides can be used in cancer treatment by way of triple-helix
CC   suppression of specific oncogenes including those of endogenous or viral
CC   origin. Such therapeutic oligonucleotides are capable of forming triple-
CC   helices with such sequences in cancerous cells containing the activated
CC   oncogene, so preferentially killing or repressing the cancer causing
CC   cell. The present sequence represents an oligonucleotide used in the
CC   methods of the present invention
XX
SQ   Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

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Qy   550 TTTTCTCTTTTCTCT 563
         |||||||||||||||
Db     2 TTTTCTCTTTTCTCT 15
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Query Match   2.1%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 3
AAH20313
ID   AAH20313/c
AC   AAH20313;
XX
DT   31-JUL-2001 (first entry)
DT   AAH20313 standard; DNA; 15 BP.
XX
DE   DNA-EDTA-FE(II) probe 7.
XX
KW   Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   modified_base   5
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "Thymidine has EDTA-FE(II) covalently attached at
                     C-5"
XX
PN   US200100231 4-A1.
XX
PD   31-MAY-2001.
XX
PF   04-AUG-1998; 98US-00128732.
XX
PR   30-OCT-1987; 87US-0011592 2.

PR   16-NOV-1990; 90US-00614205.
PR   12-NOV-1993; 93US-00152250.
XX
PA   (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
PI   Dervan PB, Moser HE;
XX
DR   WPI; 2001-342909/36.
XX
     Example 2; Fig 4B; 20pp; English.
XX
CC   This invention relates to hybridisation probes which target a specific
CC   sequence within a large double-helical nucleic acid. The probe is
CC   complementary to the target sequence and contains at least one nucleotide
CC   with an attached molecule that is able to cleave double-helical DNA e.g.
CC   EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC   where the attached molecule is a label or compound that alters gene
CC   expression, are used for specific detection and/or cleavage of double-
CC   helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC   caused by viruses, genetic defects or oncogenes), for chromosomal
CC   analysis, and for the isolation and mapping of genes. The present
CC   sequence represents a probe of the invention which is used in an example
CC   illustrating how it binds to and cleaves a double stranded fragment of
CC   plasmid pDMAG10 given in AAH20315
XX
SQ   Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

```
Qy   255 AGGCAAAGGGAAA 267
         |||  ||||| |||
Db    15 AGAGAAAGAGAAA 3
```

Query Match   1.2%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%;
Matches   10; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

RESULT 4
ABK98147
ID   ABK98147/c
AC   ABK98147;
XX
DT   07-OCT-2002 (first entry)
DT   ABK98147 standard; DNA; 15 BP.
XX
DE   Triple helix forming associated oligonucleotide #30.
XX
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
KW   oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS   Synthetic.
XX
PN   US6403302-B1.
XX
PD   11-JUN-2002.
XX
PF   16-DEC-1993; 93US-00168920.
XX
PR   17-SEP-1992; 92US-00946976.
XX
PA   (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Dervan PB, Beal PA;
XX
DR   WPI; 2002-536030/57.
XX
PT   A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT   oligonucleotide which binds in parallel and antiparallel orientation,

OM nucleic - nucleic search, using sw model

```
            GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:     March 31, 2004, 14:06:04 ; Search time 0.001 Seconds
                                       (without alignments)
                                       40.200 Million cell updates/sec

Title:
Perfect score:    us09470821
Sequence:         670
                  1 aagcgcttccaagacaacgatt.........gggtttaaataaagcgcttt 670

Searched:         2 seqs, 30 residues

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:    4

Minimum DB seq length:  0
Maximum DB seq length:  200000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 20 summaries

Database :        lrng.db:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.


                              SUMMARIES

                         %
Result      Query Match
No.   Score Length DB  ID          Description
----- ----- ------ --- ----------  -----------
1     14    2.1    15  1  AAH20313  DNA-EDTA-FE(II) pr
2     14    2.1    15  1  ABK98147  Triple helix formi
3     8.2   1.2    15  1  AAH20313  Triple helix formi
4     8.2   1.2    15  1  ABK98147  DNA-EDTA-FE(II) pr
c                             ABK98147  Triple helix formi


                              ALIGNMENTS
```

RESULT 1
ID   AAH20313
AC   AAH20313;
DT   31-JUL-2001 (first entry)
DE   DNA-EDTA-FE(II) probe 7.
KW   Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   modified_base   5
FT   /*tag= b
FT   /mod_base= OTHER
FT   /note= "Thymidine has EDTA-FE(II) covalently attached at
                          C-5"
PN   US2001002314-A1.
PD   31-MAY-2001.

XX
PF   04-AUG-1998;   98US-00128732.
XX
PR   30-OCT-1987;   87US-00115922.
PR   16-NOV-1990;   90US-00614205.
PR   12-NOV-1993;   93US-00152250.
XX
PA   (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
PI   Dervan PB, Moser HE;
XX
DR   WPI; 2001-342909/36.
XX
PT   New hybridization probe for specific triplex formation with large double
PT   helices, useful e.g. for site-specific diagnostic cleavage, contains
PT   attached functional residue.
XX
PS   Example 2; Fig 4B; 20pp; English.
XX
CC   This invention relates to hybridisation probes which target a specific
CC   sequence within a large double-helical nucleic acid. The probe is
CC   complementary to the target sequence and contains at least one nucleotide
CC   with an attached molecule that is able to cleave double-helical DNA e.g.
CC   EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC   where the attached molecule is a label or compound that alters double-
CC   expression, are used for specific detection and/or cleavage of double-
CC   helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC   caused by viruses, genetic defects or oncogenes), for chromosomal
CC   analysis, and for the isolation and mapping of genes. The present
CC   sequence represents probe of the invention which is used in an example
CC   illustrating how it binds to and cleaves a double stranded fragment of
CC   plasmid pDMAG10 given in AAH20315
XX
SQ   Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

Query Match   2.1%; Score 14; DB 1; Length 15;
Best Local Similarity   100.0%;
Matches   14; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   550 TTTTCTCTTTCTCT 563
                ||||||||||||||
Db   2 TTTTCTCTTTCTCT 15

RESULT 2
ID   ABK98147
AC   ABK98147;
DT   07-OCT-2002 (first entry)
DE   Triple helix forming associated oligonucleotide #30.
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
KW   oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
OS   Synthetic.
XX
PN   US6403302-B1.
XX
PD   11-JUN-2002.
XX
PF   16-DEC-1993;   93US-00168920.
XX
PR   17-SEP-1992;   92US-00946976.
XX
PA   (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Dervan PB, Beal PA;
XX

29. US-09-477-082-2 (1-753)
    US-09-477-082-34 Sequence 34, Application US/09477082

Initial Score   =   7   Optimized Score   =   13   Significance = -0.25
Residue Identity   =   52%   Matches   =   13   Mismatches   =   12
Gaps   =   0   Conservative Substitutions   =   0

```
          580         590         600         610         620         630         640
CTGAAGGGGTTTCCTTTTATGTCTTCCACCCCACCCTTCCCCTCGCCCCTCGTTTTTGTTGGTTGTGTTTTTGTTGGTTGTTGTTTTGTTGGTTGTTCCCAAA
                                                              ||||||||   |||||
                                                          CCATATATATCTACATTCGAAAA
                                                                                   650         660         670         680         690
AAACAAGTTCTCTAAACGTTTCGGATGTGGATTCGCGGAAAAATTAACCTGCAC
|||
CAA
  X
```

30. US-09-477-082-2 (1-753)
    US-09-477-082-18 Sequence 18, Application US/09477082

Initial Score   =   6   Optimized Score   =   11   Significance = -0.26
Residue Identity   =   52%   Matches   =   11   Mismatches   =   10
Gaps   =   0   Conservative Substitutions   =   0

```
          300         310         320         330         340         350         360
CTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCCTGAGCAGTCTCCAGTTCCTCTGCTACCTTTT
                                               ||||||||||  |||||
                                           TTCTCCTTCTTTACAAACCTG
                                                                          X                  20
          370         380         390         400         410
TGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGAATACACGGACTCCCT
```

31. US-09-477-082-2 (1-753)
    US-09-477-082-22 Sequence 22, Application US/09477082

Initial Score   =   6   Optimized Score   =   10   Significance = -0.26
Residue Identity   =   43%   Matches   =   10   Mismatches   =   13
Gaps   =   0   Conservative Substitutions   =   0

```
          530         540         550         560         570         580         590
GAATCACGAATGCCCTGAGGTGCACAGCCCCTTCCCCTCTTCGGCTCCTGAAAGGGGGGTTTTCCTTTTATGTC
                                                               |||||||| |||||||||
                                                           TCCCGGGGTTTTTCCCGAGGGGGA
                                                                                 X                  20
          600         610         620         630         640
TTCCACCCCCACCCTTTCCCCTCCCTCGCCCCTCGTTTTTGTTGGTTGCCAAAAA
```

32. US-09-477-082-2 (1-753)
    US-09-477-082-30 Sequence 30, Application US/09477082

G
X

Initial Score   =   5   Optimized Score   =   11   Significance = -0.27
Residue Identity   =   50%   Matches   =   11   Mismatches   =   11
Gaps   =   0   Conservative Substitutions   =   0

```
          10          20          30          40          50          60          70
AATTAGACCGGGTATTGAAAGTAAAAGAAAAACTTCTTCCTGGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCA
||||||||  |||| |||||||||||
CGTTATATCTACATTCGAAAACGA
          10                  20 X
          80
CGTGGAGT
```

G
X
X

20. US-09-477-082-2 (1-753)
US-09-477-082-25 Sequence 25, Application US/09477082

Initial Score   =   10   Optimized Score   =   10   Significance   =   -0.23
Residue Identity   =   50%   Matches   =   10   Mismatches   =   10
Gaps   =   0   Conservative Substitutions   =   0

```
      620         630         640         650         660         670         680        X
CCCTGCCCTTCTGTTTTTGTTTTTGTCCCAAAAAACACAAGTTCTCTAAAACGTTTTCGATGTGGGATTCGCGGGAAAATTA
                                                                    |||||  |||
                                                                    GATGCAGGTGGGCGGCGGGGCTC
                                                                         10          20
```

21. US-09-477-082-2 (1-753)
US-09-477-082-21 Sequence 21, Application US/09477082

Initial Score   =   10   Optimized Score   =   14   Significance   =   -0.23
Residue Identity   =   60%   Matches   =   14   Mismatches   =   9
Gaps   =   0   Conservative Substitutions   =   0

```
      700         710         720         730
ACCTGCACCCGTTTGCAAAATGAACTTTTTTTTTTTGATCCTGTACAC
                              X
T
X
```

22. US-09-477-082-2 (1-753)
US-09-477-082-28 Sequence 28, Application US/09477082

Initial Score   =   13   Optimized Score   =   14   Significance   =   -0.23
Residue Identity   =   59%   Matches   =   13   Mismatches   =   9
Gaps   =   0   Conservative Substitutions   =   0

```
      450         460         470         480         490         500         510
AGAAGACTTTATCAATCCACTTTTTTTTTCTTTTTCATTTGCCCTGGGGGGGCCCGACGGGTTAAGTACTTTATTC
                                                              |||||  |||||
                                                              TCAAATGTTAGTTAATTTACTA
                                                                   10          20
```

23. US-09-477-082-2 (1-753)
US-09-477-082-15 Sequence 15, Application US/09477082

Initial Score   =   9   Optimized Score   =   12   Significance   =   -0.24
Residue Identity   =   54%   Matches   =   12   Mismatches   =   10
Gaps   =   0   Conservative Substitutions   =   0

```
      450         460         470         480         490
AAGACTTTATCAATCCACTTTTTTTTTCTTTTTCATTTGGCCCTGGGGGGCC
                                                   X
```

```
      520         530         540         550         560
TGTCAATTCTGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCT
                                                   X
```

```
      380         390         400         410         420         430         440        X
CCTCCAAGCTTCCCGCCGCCTTCGGAATGCAGAATACACGGGACTNCCCTTCTGTGGGACCCGGTTTGGGAGAGTCCAG
                                            |||||  |||||
                                            GTGAATAGTTTTGCAGGAGGCGAT
                                                 10          20
```

```
      170         180         190         200         210         220         230        X
TTCAACAGGAAAACCACAATATTTTTGTTTCCTTGACTTCCTCTAGAAACAGGGCTGTGTGGGGTGGGGAAGCAA
                                                                    |||||  ||||
                                                                    GCCTACAGGTGGGTGGAGAACTC
                                                                         10          20
```

```
      240         250         260         270         280
CTTGGGATCTGCCCTTCTGAGGACACCTTCGGTGTGCCTGGGCCCAGGTCT
```

24. US-09-477-082-2 (1-753)
US-09-477-082-16 Sequence 16, Application US/09477082

Initial Score   =   8   Optimized Score   =   9   Significance   =   -0.24
Residue Identity   =   45%   Matches   =   9   Mismatches   =   11
Gaps   =   0   Conservative Substitutions   =   0

```
      120         130         140         150         160         170        X
GGTGCCAGAAAGGGTGGACGGGGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGATAGAAACCACAATATT
                                                                   |||||   ||||
                                                                   CCCAACCACAAAAGGGTCATG
                                                                        10          20
```

```
      190         200         210         220         230
TTTGTTTCTTGACTTGCTCTAGAAACAGGGCTGTGTGGGGGTGGGGAAGC
```

25. US-09-477-082-2 (1-753)
US-09-477-082-23 Sequence 23, Application US/09477082

Initial Score   =   8   Optimized Score   =   9   Significance   =   -0.24
Residue Identity   =   42%   Matches   =   9   Mismatches   =   12
Gaps   =   0   Conservative Substitutions   =   0

```
      290         300         310         320         330         340        X
TCTCCTGTGTGGTTTCTCTCGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTTCTGAGCAGTCTCCAGTTT
                                                            |||||  |||||
                                                            TCACAGGTAGTCACGGAGAAAACC
                                                                 10          20
```

```
      360         370         380         390         400
CCTCTGCTACCTTTTTGTTCCTCCCAAGCTTCCCTGGCGCCTTCGGAATGCAG
```

26. US-09-477-082-2 (1-753)
US-09-477-082-20 Sequence 20, Application US/09477082

Initial Score   =   8   Optimized Score   =   11   Significance   =   -0.24
Residue Identity   =   52%   Matches   =   11   Mismatches   =   10
Gaps   =   0   Conservative Substitutions   =   0

```
      190         200         210         220         230         240         250        X
TTCTTGACTTGCTCTAGAAAACAGGGCTGTGTGGGGGTGGGGAAGCAACTTGGATCTGCCCTTCTGAGGACACCT
                                                                    |||||  |||||
                                                                    TTTGCCTTATCTGAGGAGAGA
                                                                         10          20
```

27. US-09-477-082-2 (1-753)
US-09-477-082-17 Sequence 17, Application US/09477082

Initial Score   =   12   Optimized Score   =   14   Significance   =   -0.24
Residue Identity   =   66%   Matches   =   14   Mismatches   =   7
Gaps   =   0   Conservative Substitutions   =   0

```
      60          70          80          90          100         110         120        X
CCCCCTTCCCTGCTGAGACACGTGGAGTTAGGCAGTTAGGGGACTCGGACTGGCATGGTTGGCCAGGAAAGG
                                                                   |||||   |||
                                                                   GATGACATGGTGCCTGGGAAC
                                                                        10          20
```

```
      270         280         290         300
CTGGTGCTGCCTGGCCCAGGGTCTCCTGTGTGGTTTCTCTGTCTGAGCCGAT
```

28. US-09-477-082-2 (1-753)
US-09-477-082-32 Sequence 32, Application US/09477082

```
      130         140         150         160         170
GTGGAGCGGGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAAC
```

13. US-09-477-082-2 (1-753)   Sequence 13, Application US/09477082

```
Initial Score          = 13   Optimized Score = 16   Significance = -0.21
Residue Identity        = 80%  Matches         = 16   Mismatches   = 4
Gaps                    = 0    Conservative Substitutions = 0
```

14. US-09-477-082-31   Sequence 31, Application US/09477082

```
Initial Score          = 13   Optimized Score = 17   Significance = -0.21
Residue Identity        = 80%  Matches         = 17   Mismatches   = 4
Gaps                    = 0    Conservative Substitutions = 0
```

15. US-09-477-082-19   Sequence 19, Application US/09477082

```
Initial Score          = 13   Optimized Score = 14   Significance = -0.21
Residue Identity        = 63%  Matches         = 14   Mismatches   = 8
Gaps                    = 0    Conservative Substitutions = 0
```

16. US-09-477-082-14   Sequence 14, Application US/09477082

```
Initial Score          = 13   Optimized Score = 13   Significance = -0.21
Residue Identity        = 56%  Matches         = 13   Mismatches   = 10
Gaps                    = 0    Conservative Substitutions = 0
```

17. US-09-477-082-27   Sequence 27, Application US/09477082

```
Initial Score          = 12   Optimized Score = 15   Significance = -0.21
Residue Identity        = 62%  Matches         = 15   Mismatches   = 9
Gaps                    = 0    Conservative Substitutions = 0
```

18. US-09-477-082-24   Sequence 24, Application US/09477082

```
Initial Score          = 11   Optimized Score = 11   Significance = -0.22
Residue Identity        = 50%  Matches         = 11   Mismatches   = 11
Gaps                    = 0    Conservative Substitutions = 0
```

19. US-09-477-082-26   Sequence 26, Application US/09477082

```
Initial Score          = 11   Optimized Score = 13   Significance = -0.22
Residue Identity        = 56%  Matches         = 13   Mismatches   = 10
Gaps                    = 0    Conservative Substitutions = 0
```

9. US-09-477-082-2 (1-753)
US-09-477-082-6 Sequence 6, Application US/09477082

Initial Score =	25	Optimized Score = 81 Significance = -0.11
Residue Identity =	37%	Matches = 86 Mismatches = 140
Gaps =	2	Conservative Substitutions = 0

```
510          520          530          540          550          560          570          580
TTCTGTCATTCTGTCGAATCACGAAATGCCTGAGGTGGCACAGCCCCTTTCCCTCTTTCGGTTCCTGAAGGG
ATCATCACCTCAAACAGAGAAATATCCCGGATGAGGCTGACTTTCTGCTGGGGATGGCCACTGTGAATAACTG
450          460          470          480          490          500          510
 
590          600          610          620          630          640          650
GTTTTCCTTTATGTCTTCCACCCCCTCCCCTCCCTGCCCTCGTTTTTGTTGTTGCCAAAAAACAAGT
TGTTCCTACCGAAAACCTGCGAGAGGGAACCCTGGTACATCCACTTTGCCAGAGGCCTGAGAGCGGATGT
520          530          540          550          560          570          580
 
660          670          680          690          700          710
TCTCTAAACGTTTTCGAGATGTGGA------TTCGCGGAAAATTAAACCTGCACCCGGTTTGCAAAATGAACTTTT
CCTCCGGGTTAAGTTTGCTCTACTCAGCCCTCCTCACTGTTACACTACCTTCCAATCACACTACT
600          610          620          630          640          650          660
 
720          730          740          750    X
TTTTTTTTTGATCCGTGTACACTGGTTTTTTTTTAACCTT
AATCTACTCAATTATTCAGAGACGCCTATTAGAAAGTGCTAATGTCAGATTTAGATCACATTAACAGGTCAGAGAACTGTC
670          680          690          700          710          720          730
 
CAAGGGGAGTGG
740
```

10. US-09-477-082-2 (1-753)
US-09-477-082-33 Sequence 33, Application US/09477082

Initial Score =	21	Optimized Score = 21 Significance = -0.15
Residue Identity =	100%	Matches = 21 Mismatches = 0
Gaps =	0	Conservative Substitutions = 0

```
40           50           60           70           80           90           100
GGGAGCCTTTCCCACCCCCTTCCCTGCTCAGCACGTGAGTTAGGGGACTCGGAGACTGCGAT
                                                               |||||||||||||||||||||
40           50           60           70           80           90           100
```

11. US-09-477-082-2 (1-753)
US-09-477-082-29 Sequence 29, Application US/09477082

Initial Score =	19	Optimized Score = 19 Significance = -0.16
Residue Identity =	90%	Matches = 19 Mismatches = 2
Gaps =	0	Conservative Substitutions = 0

```
40           50           60           70           80           90           100        X
GGGAGCCTTTCCCACCCCCTTCCCTGCTCAGCACGTGGCACGTGGAGGTTAGGGAGCAGGTTAGGGGACTCGGAGAGACTGCGGAT
                                                              |||||||||||||||||||||
GGTGCCAGGAAAAGGGTGGAGCGGGGTGAGTGCCTGTTGCCAAGGTGGCCT        TAGGGGACTCGGAGACTGCGA
120          130          140          150          160                    10        20
```

12. US-09-477-082-2 (1-753)
US-09-477-082-8 Sequence 8, Application US/09477082

Initial Score =	19	Optimized Score = 236 Significance = -0.16
Residue Identity =	33%	Matches = 252 Mismatches = 501
Gaps =	9	Conservative Substitutions = 0

```
X            10           20           30           40           50           60
AATTAGACCGCGTATTGAAAG---TAAAAGAAAACTTCTTCCTGGAGAGCCTTTCCCACCCCCTTCCCTGCTGA
AATATTAATAATAGTGCAAAAGTTCCTCACTCAGGAGCGCCCAGGTAATTGGGGACACTTTACACAGGGGCAGA
X            10           20           30           40           50           60           70
 
70           80           90           100          110          120          130          140
GCACGTGGAGTTAGGCAGGTTAGGGGACTTCGGACGATGGGTGCCAGCAGAAAAGGGTGGAGCGGGGTGAGTG
AGTCTGAGAGGTTCCTGTGTGTGAAGGAAAAATAGGTAGAAACTAGTTCTTCGGAGGAAAACGACCCGAGTTGGGGTG
80           90           100          110          120          130          140
 
150          160          170          180          190          200          210
CCTGTTGCCAAGGTGGCCTTCTTCAAACAGGAAAACCACAAATATTTTGTTCTTTG-ACTTGCTTAGAAATCAGG
GTGCAAATGGAAAGCAAGTCCTCTTACTAGGAGAGTGTTGTTTTGTTTTACATCTCTAGTGTTTGACCCACAGAGTCA
150          160          170          180          190          200          210
 
220          230          240          250          260          270          280
GCACGTGTGGAGTTAGGCAGGTTAGGGGACTTCGGACGATGGGTGCCAGCAGAAAAGGGTGGAGCGGGGTGAGTG
GCTTCCTGGGGTTGGGGTTTTTGGTAATTCCAGACAGTTTGCCAAAATGAAAAGCAAACCTCGGGGGATA
220          230          240          250          260          270          280
 
290          300          310          320          330          340          350
CTGTCTGAATCAACAATCACAAATTTTGCAAAAAGCACGGAGAAAGTGCCCAAACTTCAGAGCAATTAGGG
GCTTCCTGGGGTTGGGGTTTTTGGTAATTCCAGACAGTTTGCCAAAATGAAAAGCAAACCTCGGGGGATA
290          300          310          320          330          340          350
 
360          370          380          390          400          410          420
TCCTTCTGCTACCTTTTNCTCCTTCCAAGCTTCCCTGCGCCTCGAATGCCAGATACACGGACTCCCCTTCCTGTGG
ACAGGAAGTGGGACACACATCTTGGTATGCAGCGTGGGCGGGCGGGCTCGGTGCCGGCCGGGCCAGGAAATGGG
290          300          310          320          330          340          350
 
430          440          450          460          470          480          490
ACCCGGTTGGAGAGTCCAGAAGACTTTATCAAATCCACTTTTTTTTTCTTTTTCATTTGGCCCTGGGGCCGGAC
AGAAAAATCCTTCTTATGCCTATTTTTTTTAAATCAAAAGAAGGGATTTNAACATGACTTAACACAAAAAGGGCCATG
430          440          450          460          470          480          490          500
```

6. US-09-477-082-2 (1-753)
US-09-477-082-5 Sequence 5, Application US/09477082

Initial Score =	31	Optimized Score = 122 Significance = -0.07
Residue Identity =	32%	Matches = 131 Mismatches = 264
Gaps =	2	Conservative Substitutions = 0

7. US-09-477-082-2 (1-753)
US-09-477-082-10 Sequence 10, Application US/09477082

Initial Score =	30	Optimized Score = 79 Significance = -0.08
Residue Identity =	38%	Matches = 85 Mismatches = 134
Gaps =	4	Conservative Substitutions = 0

8. US-09-477-082-2 (1-753)
US-09-477-082-9 Sequence 9, Application US/09477082

Initial Score =	30	Optimized Score = 228 Significance = -0.08
Residue Identity =	36%	Matches = 260 Mismatches = 429
Gaps =	15	Conservative Substitutions = 0

4. US-09-477-082-2 (1-753)
   US-09-477-082-3 Sequence 3, Application US/09477082

Initial Score   = 35   Optimized Score = 236   Significance = -0.04
Residue Identity   = 36%   Matches   = 305   Mismatches   = 448
Gaps   = 84   Conservative Substitutions = 0

5. US-09-477-082-2 (1-753)
   US-09-477-082-7 Sequence 7, Application US/09477082

Initial Score   = 31   Optimized Score = 64   Significance = -0.07
Residue Identity   = 39%   Matches   = 69   Mismatches   = 102
Gaps   = 3   Conservative Substitutions = 0

2. US-09-477-082-2 (1-753) Sequence 4, Application US/09477082
   US-09-477-082-4

Initial Score	=	65	Optimized Score	=	216	Significance	=	0.19
Residue Identity	=	35%	Matches	=	242	Mismatches	=	416
Gaps	=	25	Conservative Substitutions	=	0			

3. US-09-477-082-2 (1-753) Sequence 1, Application US/09477082
   US-09-477-082-1

Initial Score	=	36	Optimized Score	=	219	Significance	=	-0.03
Residue Identity	=	36%	Matches	=	243	Mismatches	=	424
Gaps	=	5	Conservative Substitutions	=	0			

Seg Id 2 VS. all to help locate primers

```
> O <
O | O    IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09477082-2vs09477082-_.res made by spaul on Wed 31 Mar 104 14:27:27-PST.

Query sequence being compared:US-09-477-082-2 (1-753)
Number of sequences searched: 32
Number of scores above cutoff: 32

Results of the initial comparison of US-09-477-082-2 (1-753) with:
File : US09477082.seq

SCORE													
STDEV	0	84	167	251	335	418	502	586	669	753			
	0	1	2	3	4	5							

SEARCH STATISTICS

Scores:
	Mean	Median
	40	13

	Standard Deviation
	130.74

Times:
	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

PARAMETERS

Similarity matrix   Unitary
		K-tuple	Joining penalty	Window size
Mismatch penalty	1	4	30	500
Gap penalty	5.00			
Gap size penalty	0.33			
Cutoff score	0			
Randomization group	1			

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Score	Opt. Score	Sig.	Frame

1. US-09-477-082-2 Sequence 2, Application US   753   753   5.45   0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
2. US-09-477-082-4	Sequence 4, Application US	659	65	216	0.19	0
3. US-09-477-082-1	Sequence 1, Application US	670	36	219	0.03	0
4. US-09-477-082-3	Sequence 3, Application US	879	35	236	0.04	0
5. US-09-477-082-7	Sequence 7, Application US	177	31	64	0.07	0
6. US-09-477-082-5	Sequence 5, Application US	448	31	122	0.07	0
7. US-09-477-082-10	Sequence 10, Application US	223	30	79	0.08	0
8. US-09-477-082-9	Sequence 9, Application US	771	30	228	0.08	0
9. US-09-477-082-6	Sequence 6, Application US	228	25	81	0.11	0
10. US-09-477-082-33	Sequence 33, Application US	21	21	21	0.15	0
11. US-09-477-082-29	Sequence 29, Application US	21	19	21	0.16	0
12. US-09-477-082-8	Sequence 8, Application US	784	19	236	0.16	0
13. US-09-477-082-13	Sequence 13, Application US	20	13	16	0.21	0
14. US-09-477-082-31	Sequence 31, Application US	21	13	17	0.21	0
15. US-09-477-082-19	Sequence 19, Application US	22	13	14	0.21	0
16. US-09-477-082-14	Sequence 14, Application US	23	13	13	0.21	0
17. US-09-477-082-27	Sequence 27, Application US	24	13	15	0.21	0
18. US-09-477-082-24	Sequence 24, Application US	22	11	11	0.22	0
19. US-09-477-082-26	Sequence 26, Application US	23	11	13	0.22	0
20. US-09-477-082-25	Sequence 25, Application US	20	11	11	0.23	0
21. US-09-477-082-21	Sequence 21, Application US	23	10	14	0.23	0
22. US-09-477-082-28	Sequence 28, Application US	22	9	12	0.24	0
23. US-09-477-082-15	Sequence 15, Application US	22	9	13	0.24	0
24. US-09-477-082-16	Sequence 16, Application US	21	8	9	0.24	0
25. US-09-477-082-23	Sequence 23, Application US	21	8	8	0.24	0
26. US-09-477-082-20	Sequence 20, Application US	21	8	11	0.24	0
27. US-09-477-082-17	Sequence 17, Application US	23	7	14	0.24	0
28. US-09-477-082-32	Sequence 32, Application US	25	6	13	0.25	0
29. US-09-477-082-34	Sequence 34, Application US	21	6	12	0.26	0
30. US-09-477-082-18	Sequence 18, Application US	21	6	11	0.26	0
31. US-09-477-082-22	Sequence 22, Application US	23	6	11	0.26	0
32. US-09-477-082-30	Sequence 30, Application US	22	5	11	0.27	0

1. US-09-477-082-2 (1-753)   Sequence 2, Application US/09477082

Initial Score	= 753	Optimized Score	= 753	Significance	= 5.45
Residue Identity	= 100%	Matches	= 753	Mismatches	= 0
Gaps	= 0	Conservative Substitutions	= 0		

```
                10         20         30         40         50         60         70
X       AATTAGACACCGCGTATTGAAAGTAAAAAGAAAACTTCTTCCTGGGGAGCCCTTTCCCACCCCCCTTCCCTGCTGAGCA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
X       AATTAGACACCGCGTATTGAAAGTAAAAAGAAAACTTCTTCCTGGGGAGCCCTTTCCCACCCCCCTTCCCTGCTGAGCA
                10         20         30         40         50         60         70

                80         90        100        110        120        130        140
        CGTGGAGTTAGGCGAAGCAAGTTAGGGGACTCGGAGACTGGTGCCAGGAAGAGGGTGGAGCGCGGGTGAGTGCCT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CGTGGAGTTAGGCGAAGCAAGTTAGGGGACTCGGAGACTGGTGCCAGGAAGAGGGTGGAGCGCGGGTGAGTGCCT
                80         90        100        110        120        130        140

               150        160        170        180        190        200        210
        GTTGCCAAGGTGGCCTCTTCAACAGGAAAACCACACAATATTTTTGTTTTTGTTCTTGCTCTAGAAACACAGGCTG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GTTGCCAAGGTGGCCTCTTCAACAGGAAAACCACACAATATTTTTGTTTTTGTTCTTGCTCTAGAAACACAGGCTG
               150        160        170        180        190        200        210

               220        230        240        250        260        270        280
        TGGGGGGTGGGGAAGCAACTTGGGATTCTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGCCCAGGTCTCCTGT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TGGGGGGTGGGGAAGCAACTTGGGATTCTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGCCCAGGTCTCCTGT
               220        230        240        250        260        270        280

               290        300        310        320        330        340        350        360
        GTGGGTTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTCACTCTTGAGCAGTCTCCAGTTCCTCTGCT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GTGGGTTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTCACTCTTGAGCAGTCTCCAGTTCCTCTGCT
               290        300        310        320        330        340        350        360
```

T
X

30. US-09-477-082-1 (1-670)
US-09-477-082-32 Sequence 32, Application US/09477082

Initial Score	=	6	Optimized Score	=	12	Significance = -0.24
Residue Identity	=	48%	Matches	=	12	Mismatches = 13
Gaps	=	0	Conservative Substitutions	=	0

```
           110        120        130        140        150  X     160        170
GAGCAGGGCTAAGCCAAGTACGAATGAACCAGACCACCACTTCCTTTTTTTTCTGAACGATCTACCCGCAATTT
                                                 X      |||||||||||||X
                                                 CCATATATATCTTACATTCAAAAA
                                                           X    10         20
```

31. US-09-477-082-1 (1-670)
US-09-477-082-13 Sequence 13, Application US/09477082

CAGCCACAGGGGCTGACTTTACCCAGTCCGGCGGGAGGGAGGAGGAGGAGAGAGGCTGGTC
| |
CAA
X

Initial Score	=	5	Optimized Score	=	9	Significance = -0.25
Residue Identity	=	45%	Matches	=	9	Mismatches = 11
Gaps	=	0	Conservative Substitutions	=	0

```
          180        190        200        210        220
           10        X 30          40       X 50          60         70
AAGCGGCTCCAAGACACCGATTGCAGAAGGAGAACACGGGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGAT
                    ||||||
                    GGTGGAGCGCGGGGTGTGGGGTCG
                  X          10            20
```

32. US-09-477-082-1 (1-670)
US-09-477-082-31 Sequence 31, Application US/09477082

GGGAACTCAGCCTGAGCACGGGTT
    80   90

Initial Score	=	5	Optimized Score	=	9	Significance = -0.25
Residue Identity	=	42%	Matches	=	9	Mismatches = 12
Gaps	=	0	Conservative Substitutions	=	0

```
           280        290        300        310        320        330
CCTATTCCCAGACCCTTGCAAGAAAGAAATGGCATATTACTTGCCCGCCGACAGGGGGTTATTTATTACTAAAATG
                                           ||||||   ||||||||||X
                                        TAGGGGATTIGGAGATTGTTGA
                                                 X   10         20
```

```
           350        360        370        380        390
GAGTCAGTATATAAATGCTTTCCAATAAAGCATGTCCAGCGCTCGGGCTTT
```

280   290   300   310
CTATTCCCAGACGACCCTTTGCAAGAAGAAAATGGCATATTACTTGCCGCCG

22. US-09-477-082-1 (1-670)
    US-09-477-082-29 Sequence 29, Application US/09477082

Initial Score   =   7   Optimized Score   =   8   Significance   =   -0.23
Residue Identity =   38%   Matches   =   8   Mismatches   =   13
Gaps   =   0   Conservative Substitutions =   0

TGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCGGAGACCAGATT
510   520   530   540   550   X   560   X   570   X
CTGCCTTTACGCTGGAGGAAGTGTTTTTCACAGGTTCTCCTCTTTAT
580   590   600   610   620

                                              TAGGGGATTCGGAGAGATTGCGA

23. US-09-477-082-1 (1-670)
    US-09-477-082-17 Sequence 17, Application US/09477082

Initial Score   =   7   Optimized Score   =   9   Significance   =   -0.23
Residue Identity =   42%   Matches   =   9   Mismatches   =   12
Gaps   =   0   Conservative Substitutions =   0

CGCTCCAAGACACGATTGCAGAAGGAACACGGGTGGCCACTGAAATTTGAAGAACACAGGGCCAAGGATGGG
10   20   30   40   50   60   70   X
AACTCAGCCTGAGCACGGGTGATCCGGAGCAGGGCTAAGCCAAGTACG
80   90   100   110   120

                            GATGACAATGGTTGCCCTGGGAAC
                                          10   20

24. US-09-477-082-1 (1-670)
    US-09-477-082-27 Sequence 27, Application US/09477082

Initial Score   =   7   Optimized Score   =   12   Significance   =   -0.23
Residue Identity =   50%   Matches   =   12   Mismatches   =   0
Gaps   =   0   Conservative Substitutions =   0

AGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCTT
490   500   510   520   530   540   550
TCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAGGAAGTGTTTTCACAGG
560   570   580   590   600   610

CT   TGTCCTTCGGTAAGTTTTTGCCTTA
X   10   20

25. US-09-477-082-1 (1-670)
    US-09-477-082-25 Sequence 25, Application US/09477082

Initial Score   =   6   Optimized Score   =   10   Significance   =   -0.24
Residue Identity =   50%   Matches   =   10   Mismatches   =   0
Gaps   =   0   Conservative Substitutions =   0

CTCCTTTTTTTCTGAACGGATCTACCCGCCATTTCAGCCACGAGGGCCTGACTTTACCCAGGGGAGGGGAG
150   160   170   180   190   200   210   X

                                  GATGCAGGTGGGCGGGGGGCTC
                                          10   20

220   230   240   250   260

GAGAGGGGCTGGTCTGTCTGTGACTTCAGTTCGCTGAGGTTTGATCAAGGCAAAG

26. US-09-477-082-1 (1-670)
    US-09-477-082-34 Sequence 34, Application US/09477082

Initial Score   =   6   Optimized Score   =   8   Significance   =   -0.24
Residue Identity =   38%   Matches   =   8   Mismatches   =   13
Gaps   =   0   Conservative Substitutions =   0

CTCTTCTGAATGGTTGGAAATTGGGCAATCTCTGTTCCTTTAAACAGGAAACACATTTCTTTGTTCGGAGTCAT
430   440   450   460   470   480   490   X

                                       CGTGTPATCTGCATTGGAGGCG
                                                  10   20

500   510   520   530   540
CTCTGTTCTGCCTTTAGGAGTAAAGTTTTACCCTGCAGTTCCTTCTGTGGT

27. US-09-477-082-1 (1-670)
    US-09-477-082-30 Sequence 30, Application US/09477082

Initial Score   =   6   Optimized Score   =   10   Significance   =   -0.24
Residue Identity =   45%   Matches   =   10   Mismatches   =   12
Gaps   =   0   Conservative Substitutions =   0

TCCGGAGCAGGGCTAAGCCAAGTACGGAATGAACCAGCACCACTTCCTCCTTTTTTTTCTGAACGGATCTACCCGC
100   110   120   130   140   150   170

                                       CGTATATCTTACATTGGAAAGGA
                                                  10   20   X

.   180   190   200   210   220
ATTTCAGCCACAGGGGCTGACTTTACCCAGTCCGGCGCGGGAGGGGAGGAGGAGG

28. US-09-477-082-1 (1-670)
    US-09-477-082-21 Sequence 21, Application US/09477082

Initial Score   =   6   Optimized Score   =   11   Significance   =   -0.24
Residue Identity =   47%   Matches   =   11   Mismatches   =   12
Gaps   =   0   Conservative Substitutions =   0

GTCAGTATAAAAATGCTTTCCAATAAAAGCATGTCCAGCGCGCTCGGGCGTTAGTTGTCATTGCACGTCCATGAAATTGTCTG
350   360   370   380   390   400   410

                                       TCAAAATGTTAGTTAATTTACTA
                                                  10   20

420   430   440   450   460
CCACATCCCTCTTCTGAAATGGTTGGAAATTGGGCAATCTCTGTTCCTTTAAAC

29. US-09-477-082-1 (1-670)
    US-09-477-082-14 Sequence 14, Application US/09477082

Initial Score   =   6   Optimized Score   =   8   Significance   =   -0.24
Residue Identity =   34%   Matches   =   8   Mismatches   =   15
Gaps   =   0   Conservative Substitutions =   0

CGAATGAACCAGACCACTTCCTCCTTTTTTTCTGACGGATCTACCCGCCATTTCAGCCACGAGGGCTGACTTTA
130   140   150   160   170   180   190   X

                                       TATTTTGACTTAGATTATATTC
                                                  10   20

X   200   210   220   230   240
CCCAGTCCGGCGCGGGAGGGGAGGAGGAGGAGGGGCTGGTCTGTTGGACTTCAGTTCGCTGAG

TCTCGGGAGGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
```
                                           |||||||||||||||||||||||
                                           TTCTCCCTCCTCTTACAACCTG
                                                         10        20
```
GTTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT

14. US-09-477-082-1 (1-670)
US-09-477-082-33 Sequence 33, Application US/09477082

Initial Score   =   9   Optimized Score   =   10   Significance = -0.21
Residue Identity = 47%   Matches   = 10   Mismatches   = 11
Gaps   =   0   Conservative Substitutions =   0

TGCTTTAGGAGTAAAAGTTTACCCTGCAGTTCCTTCTTTCTTTCTCTGTGGGTGAAGTTTTCTCTTTTCTCTCGGGAGGACCAGATT
```
     510           520           530           540           550           560           570
                                                                          X                 X
                                                                TAGGGGGACTCGGAGACTGCGA
                                                                   10        20
```
CTGGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTAT
```
     580           590           600           610           620
                                                                  X
```

15. US-09-477-082-1 (1-670)
US-09-477-082-19 Sequence 19, Application US/09477082

Initial Score   =   9   Optimized Score   =   13   Significance = -0.21
Residue Identity = 59%   Matches   = 13   Mismatches   =   9
Gaps   =   0   Conservative Substitutions =   0

AGCAGGGGCTAAGCCAAGTACGAAATGAACCAGACCACTTCCTCCTCTTTTTTTTCTGAACGAATCTACCCGCCATTTC
```
     110           120           130           140           150           160           170
                                                   X                              X               X
                                                              TTCAGTAAAGTTACGCGCAAATTTC
                                                                 10        20   X
```

16. US-09-477-082-1 (1-670)
US-09-477-082-26 Sequence 26, Application US/09477082

Initial Score   =   9   Optimized Score   =   11   Significance = -0.21
Residue Identity = 47%   Matches   = 11   Mismatches   =   9
Gaps   =   0   Conservative Substitutions =   0

AGCCACAGGGCTGACTTTACCCAGTTCCGGCGGGGGAGGGAGGAGGGGCTGG
```
     180           190           200           210           220
```

17. US-09-477-082-1 (1-670)
US-09-477-082-23 Sequence 23, Application US/09477082

Initial Score   =   8   Optimized Score   =   9   Significance = -0.22
Residue Identity = 42%   Matches   =   9   Mismatches   = 12
Gaps   =   0   Conservative Substitutions =   0

CGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTTCACAGGTTCT
```
     570           580           590           600           610
                       X                                       X
```
G
X

CTCTTCTTCTCGGGAGGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTAT
```
     560           570           580           590           600           610           620
                                                                                    X
```

TCACAGGTTAGCACGGAAAACC
```
                X
                10        20
```

18. US-09-477-082-1 (1-670)
US-09-477-082-24 Sequence 24, Application US/09477082

Initial Score   =   8   Optimized Score   =   12   Significance = -0.22
Residue Identity = 54%   Matches   = 12   Mismatches   = 10
Gaps   =   0   Conservative Substitutions =   0

CTTTTGTGTTTTTTTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT
```
     630           640           650           660           670
```

19. US-09-477-082-1 (1-670)
US-09-477-082-15 Sequence 15, Application US/09477082

Initial Score   =   8   Optimized Score   =   11   Significance = -0.22
Residue Identity = 50%   Matches   = 11   Mismatches   = 11
Gaps   =   0   Conservative Substitutions =   0

ACGGGGTGGCCAACTGAAAATTTGAAGAAGACAGGGCAAGGATGGGGAACTCAGCCCTGAGCACGGGTTGAATCCGG
```
      40            50            60            70            80            90           100
                                                                              X             X
                                                          GCCTTACAGGGTGGGGTGGAAAACTC
                                                             10        20   X
```

20. US-09-477-082-1 (1-670)
US-09-477-082-22 Sequence 22, Application US/09477082

Initial Score   =   8   Optimized Score   = 11   Significance = -0.23
Residue Identity = 47%   Matches   = 11   Mismatches   = 12
Gaps   =   0   Conservative Substitutions =   0

GCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGTGTTTTTTTTCGAGCCATG
```
     580           590           600           610           620           630           640           650
                                                          X                                       X
                                                                 TCCCGGGGTTTCCCGGAGGGGA
                                                                    10        20
```

21. US-09-477-082-1 (1-670)
US-09-477-082-16 Sequence 16, Application US/09477082

Initial Score   =   7   Optimized Score   =   9   Significance = -0.23
Residue Identity = 45%   Matches   =   9   Mismatches   = 11
Gaps   =   0   Conservative Substitutions =   0

TCCGGGCGGGAGGGAGGGAGAGGGCTGGGTCTGTGACTTCAGTGCTGAGGTTTGATCAAGGGCAAAGGGAAACTTC
```
     200           210           220           230           240           250           260
                                                                                    X
                             CCCAACCACAAAAGGGTCATG
                                10        20
```
G
X
GGGGTTAAATAAAGCGCTTT
```
     660           670
```

CGGGTTGATCCGGAGGAGGGCTTAAGCTAACTACGAATGAACCAGA--CCACTTCCTCCGTTTTTTTCTGAACGA
          |||||
ATCTATGACATTTGAA------AATCTACCAACTCAATGGACCCAGTAACATGGACTGCTTCATCTGCTGTA
170   180   190   200   210   220   230

TCTACCCGGCCATTTCAGCCACACAGCTGACTACTTTACCCAGTCCGGCGGAGGAGGGGAGAAGGGCTGGGTCTGTGAC
   |||
TCCTCTCCATGGAGACAAAGGGGCATCAGCTATGGCAACAGGAGCCCCCATCCTATGGAGCTGGACAT
170   180   190   200   210   220   230

TTCAGTGCTGAGGGTTGATCAGGAGGGAAAACTTCCTATTCCAGTCAGTCAGTAAATGGATCGATAAAATGGTTTTCCAATAAAGCATGGCAT
  |||
CTCAGTTCACTGGTTTGA--AGTGCCCCTTCCTTGCTGGAAAACCCAAAGCGTTTTTTTATTCAGGATTGTCA
240   250   260   270   280   290   300

ATTACTTGCCGCGACACAGGGGGTTATTTATTACTAAATGGAGTCAGTATAAAATGCTTTTCCAATAAAGCATGTCC
   |||
GGGGGATAACTACCAGAAAAGGGTATACCTTGTTGAGACTGAATTCAGAGGAGCAACCCTTATTTAGAAAATGGATTT
310   320   330   340   350   360   370

AGGGCTCGGGCTTTAGTTTGCACGTTCCATGAGAATTGCTGCCACATCCCTTCTTCTGAATGGTTGGGAATAACT
   |||
ATC-ATCACCTCAAACGAAGCATATATCCCGGATGGAGGCTGACTTTCTGCTGGGGATGGCCACTGTGAATAACT
380   390   400   410   420   430   440

ACTCTCTGTTCCTTTAAACAGGAAACANTTTCTTGTTCGGAGTGAGTCATCTCTGTTCTCGCCTTTAGGAGTAAAGT
   |||
GTGTTCCTACCCGAAACCCTGCAGAGGGAACCCTGGTACATCCAGTCACTTTGCCCACTGTCAGAGGACGGGATG
450   460   470   480   490   500   510   520

TTACCCTCGACTTCCTTCTGTGGTGAAGTTTTTCTCTTCGGAGACCCACTGTTACAC------TACTTCCCCCTACTCATCAC
   |||
TCCTCGGGTAAGTTTGCTTCAGCCCCTCCTCCACTGTTACAC------TACTTCCCCCTACTCATCAC
530   540   550   560   570   580   590   600

GGAAGTGTTTTCACAGGTTCTCCTCCTTTATCCTTTTGTGTTTTTTTTTCGAGCCCATGGGGGTTAAATAAAGC
   |||
ACTACTACTCATTAATTCAGAAGACCCTAGTTGTAGACAGGTTCACATTAACADGTCAGAGA
600   610   620   630   640   650   660   670

GCTTT
|||||
ACTGTCAAAGGGGAGTGTTTCGGTTCAACTCTAAAATGTCTAG
660   670   680   690   700   710   720   730

730
X

10. US-09-477-082-1 (1-670)
US-09-477-082-5 Sequence 5, Application US/09477082

Initial Score = 17	Optimized Score = 130	Significance = -0.15
Residue Identity = 33%	Matches = 144	Mismatches = 271
Gaps = 17	Conservative Substitutions = 0	

GCTTT   740   750   760   770

CGGGGAGGAGGAGAGGGCTTGGGTTCTGTGACTTTGATCAAGGAGGGAAAACTTGGAGCGATT
   |||
CCCAGACCCTTTGCAAGAAAAGAATGGCATATATTACTTGCCGCGACAGGGGGTTATTATTACTAAATGGAGTCA
210   220   230   240   250   260   270

CCCAGACCCTTTGCAAGAAAAGAATGGCATATATTACTTGCCGCGACAGGGGGTTATTATTACTAAATGGAGTCA
   |||
TGGCTTCTCCTTTATCCTTTCGTCTTTCTGGGCCCAGAAAATGGAATGCGTTCCCTAGCCTG
280   290   300   310   320   330   340

GGGGACTGGGGTGACATCTGACA
X
10   20

---

11. US-09-477-082-1 (1-670)
US-09-477-082-28 Sequence 28, Application US/09477082

GTATAAAATGCTTTTCCAATAAAGCATGTCAGCGCTCGGGCTTTAGTTTGCACGTTCCATGAATTGTGTGCCAC
   |||
CTGGCTGGTGAGAGACTGAGAGAGGCAGAAAACTGTCAGAAAACTTGGAAGCAAGGGCAGAGGGTTCCTTG--GTTGGAAAATT
100   110   120   130   140   150   160

ATCCCTGTTCTGAATGGTTGGAAATTGGGACCATCTCTGTTGTTCTTTAAACAACATGGCTGAAAAACACTTTTCTTGTTTCAGGTGAG
   |||
GGAAATTAAAGAAAACTAAAACTAAAAAAACCAGTGAGCGTCATCTGGAACGACTTTTATTTCCCTCCT
170   180   190   200   210   220   230   240

CTTTACAACCTGCTTGGAGTATATTTTTTCATAGAGATGGGAGAGAGGGGTCATCCTGGGATACTTACGGTAGGGTTTCACAGTTTTCTCTCT
   |||
TCATCTCGTTCTGCTTTAGGAGTGAGTTTTACCCGTGCAGTTCCTTTCCTTAAACAACAGAAGTTTTCATGGTTTTTCTCTCT
240   250   260   270   280   290   300

GGAGACCAGAATTCTGACTTTTACGGTCGGAGGG---------------AAGTGTTTTTCGACAGGTTCTCCTCCT
   |||
TGAAAGAAGTCGTGCCCCAAATCAACAGAAGCCTTGCTGAAAGATAATCAACGACTATGAAGGAATTCAGCAAAG
310   320   330   340   350   360   370   380

TTTTATCTTTTTGTGTTTTTTTTCTGAGCCCATGGGGGTTAAATAAAGCGCTTT
   |||
TACCGCAAATTTCCTATCTTTTTTAACGGCACATAGGTTCAGAAGGGGGGCGCCCAGCTCGATAATCTGG
390   400   410   420   430   440

630   640   650   660
X

Initial Score = 12	Optimized Score = 12	Significance = -0.19
Residue Identity = 54%	Matches = 12	Mismatches = 10
Gaps = 0	Conservative Substitutions = 0	

---

12. US-09-477-082-1 (1-670)
US-09-477-082-20 Sequence 20, Application US/09477082

GGAAGTGTTTTCACAGGTTCTCCTCCTTTATCCTTTTGTGTTTTTTTTTCGAGCCCATGGGGGTTAAATAAAGCGGAT
   |||
ATCAAGGCAAAGGGAAAACTTCCTATTCCCAGACCCTTTGCAAGAAAAGAAT
260   270   280   290   300

GTGAATAGTTTTGCAGAGGCGAT
X
10   20

Initial Score = 11	Optimized Score = 14	Significance = -0.20
Residue Identity = 66%	Matches = 14	Mismatches = 7
Gaps = 0	Conservative Substitutions = 0	

---

13. US-09-477-082-1 (1-670)
US-09-477-082-18 Sequence 18, Application US/09477082

CCTGCAGTTCCTTCTGTGGTGAAGTTTTTCTTCTTCGGAGGACCAGATTCTGCCTTTACGGCTGGAGGGAA
   |||
GGGGAGGAGGAGAGGGCTTGGGTTCTGTGACTTTGATCAAGGAGGGAAAACTTGGAGC
530   540   550   560   570   580   590

600   610   620   630   640
TTGGCCTTTATCTGAGAGAGA
X
10   20

Initial Score = 10	Optimized Score = 15	Significance = -0.21
Residue Identity = 71%	Matches = 15	Mismatches = 6
Gaps = 0	Conservative Substitutions = 0	

570   580   590   600   610   620
X

7. US-09-477-082-1 (1-670)
US-09-477-082-8 Sequence 8, Application US/09477082

Initial Score   = 25   Optimized Score   = 220   Significance = -0.08
Residue Identity   = 36%   Matches   = 247   Mismatches   = 420
Gaps   = 13   Conservative Substitutions = 0

8. US-09-477-082-1 (1-670)
US-09-477-082-10 Sequence 10, Application US/09477082

Initial Score   = 24   Optimized Score   = 222   Significance = -0.09
Residue Identity   = 37%   Matches   = 255   Mismatches   = 402
Gaps   = 5   Conservative Substitutions = 0

9. US-09-477-082-1 (1-670)
US-09-477-082-9 Sequence 9, Application US/09477082

Initial Score   = 22   Optimized Score   = 222   Significance = -0.10
Residue Identity   = 37%   Matches   = 255   Mismatches   = 402
Gaps   = 18   Conservative Substitutions = 0

4. US-09-477-082-4 Sequence 4, Application US/09477082

Initial Score = 33	
Optimized Score = 210	Significance = -0.01
Residue Identity = 36% Matches = 231	Mismatches = 399
Gaps = 11 Conservative Substitutions = 0	

5. US-09-477-082-6 Sequence 6, Application US/09477082

Initial Score = 31	
Optimized Score = 80	Significance = -0.03
Residue Identity = 37% Matches = 86	Mismatches = 142
Gaps = 4 Conservative Substitutions = 0	

6. US-09-477-082-7 Sequence 7, Application US/09477082

Initial Score = 25	
Optimized Score = 62	Significance = -0.08
Residue Identity = 35% Matches = 62	Mismatches = 115
Gaps = 0 Conservative Substitutions = 0	

2. US-09-477-082-1 (1-670)
US-09-477-082-3 Sequence 3, Application US/09477082

Initial Score	=	46	Optimized Score = 222	Significance = 0.10
Residue Identity	=	36%	Matches = 250	Mismatches = 418
Gaps	=	18	Conservative Substitutions = 0

3. US-09-477-082-1 (1-670)
US-09-477-082-2 Sequence 2, Application US/09477082

Initial Score	=	36	Optimized Score = 219	Significance = 0.02
Residue Identity	=	36%	Matches = 243	Mismatches = 424
Gaps	=	5	Conservative Substitutions = 0

Seq id 1 vs all — to help locate primers
09477082-1vs09477082-_.res

```
> O <
O|/O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file 09477082-1vs09477082-_.res made by spaul on Wed 31 Mar 104 14:25:38-PST.

Query sequence being compared:US-09-477-082-_ (1-670)
Number of sequences searched:                 32
Number of scores above cutoff:                32

Results of the initial comparison of US-09-477-082-1 (1-670) with:
File : US09477082.seq
```

```
            PARAMETERS
Similarity matrix    Unitary
                       1   K-tuple           4
Mismatch penalty    5.00   Joining penalty  30
Gap size penalty    0.33   Window size     500
Gap penalty            1
Cutoff score           1
Randomization group    0

            SEARCH STATISTICS

Scores:           Mean        Median
                   34            9

Times:           CPU                  Total Elapsed
               00:00:00.00           00:00:00.00

Number of residues:            6071
Number of sequences searched:    32
Number of scores above cutoff:   32
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

```
Sequence Name   Description              Init.   Opt.
                                         Score  Score  Sig. Frame
```

```
SCORE
STDEV 0    74    149   223   298   372   447   521   596   670
      0     1     2     3     4     5     ...
```

```
1. US-09-477-082-1 Sequence 1, Application US   670   670   5.46   0

The list of other best scores is:

Sequence Name              Description                        Length Init.  Opt.
                                                                    Score  Score  Sig. Frame
 2. US-09-477-082-3  Sequence 3, Application US                879   222    46    0.10   0
 3. US-09-477-082-2  Sequence 2, Application US                753   219    36    0.02   0
 4. US-09-477-082-4  Sequence 4, Application US                659   210    33    0.01   0
 5. US-09-477-082-6  Sequence 6, Application US                228   228    31    0.03   0
 6. US-09-477-082-7  Sequence 7, Application US                177    80    25    0.08   0
 7. US-09-477-082-8  Sequence 8, Application US                784   220    25    0.08   0
 8. US-09-477-082-10 Sequence 10, Application US               223    80    24    0.09   0
 9. US-09-477-082-9  Sequence 9, Application US                771   222    22   -0.10   0
10. US-09-477-082-5  Sequence 5, Application US                448   222    17   -0.15   0
11. US-09-477-082-28 Sequence 28, Application US                22    12   130   -0.19   0
12. US-09-477-082-20 Sequence 20, Application US                21    11    14   -0.20   0
13. US-09-477-082-18 Sequence 18, Application US                21    10    15   -0.21   0
14. US-09-477-082-33 Sequence 33, Application US                21    10    15   -0.21   0
15. US-09-477-082-19 Sequence 19, Application US                21     9    13   -0.21   0
16. US-09-477-082-26 Sequence 26, Application US                23     9    11   -0.22   0
17. US-09-477-082-23 Sequence 23, Application US                23     8    11   -0.22   0
18. US-09-477-082-24 Sequence 24, Application US                22     8    12   -0.22   0
19. US-09-477-082-15 Sequence 15, Application US                22     8    10   -0.22   0
20. US-09-477-082-22 Sequence 22, Application US                23     8    11   -0.22   0
21. US-09-477-082-16 Sequence 16, Application US                20     7    11   -0.23   0
22. US-09-477-082-29 Sequence 29, Application US                21     7     8   -0.23   0
23. US-09-477-082-17 Sequence 17, Application US                21     7     8   -0.23   0
24. US-09-477-082-27 Sequence 27, Application US                24     7    12   -0.23   0
25. US-09-477-082-25 Sequence 25, Application US                20     6    10   -0.24   0
26. US-09-477-082-34 Sequence 34, Application US                21     6     8   -0.24   0
27. US-09-477-082-30 Sequence 30, Application US                22     6    10   -0.24   0
28. US-09-477-082-21 Sequence 21, Application US                23     6    11   -0.24   0
29. US-09-477-082-14 Sequence 14, Application US                23     6     8   -0.24   0
30. US-09-477-082-32 Sequence 32, Application US                25     6    12   -0.24   0
31. US-09-477-082-13 Sequence 13, Application US                20     5     9   -0.25   0
32. US-09-477-082-31 Sequence 31, Application US                21     5     9   -0.25   0
```

```
1. US-09-477-082-1 (1-670)
   US-09-477-082-1 Sequence 1, Application US/09477082

Initial Score      =   670   Optimized Score       =   670   Significance =  5.46
Residue Identity   =  100%   Matches               =   670   Mismatches   =     0
Gaps               =     0   Conservative Substitutions =   0
```

```
            10        20        30        40        50        60        70
X  AAGCGCTCCAAGACACGATTCCAGAAGGACACGGGGGTGGGTGCCAACTGAAATTTGAAGAACAGGGCCAAGAT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AAGCGCTCCAAGACACGATTCCAGAAGGACACGGGGGTGGGTGCCAACTGAAATTTGAAGAACAGGGCCAAGAT
X         10        20        30        40        50        60        70

            80        90       100       110       120       130       140
   GGGAACTCAGCCTGACCACGGGTTGATCCGGACAGGGCGTAAGCCAAGTACGAATGAACCAGACCACTTCCT
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGGAACTCAGCCTGACCACGGGTTGATCCGGACAGGGCGTAAGCCAAGTACGAATGAACCAGACCACTTCCT
          80        90       100       110       120       130       140

           150       160       170       180       190       200       210
   CCTTTTTTTCTGAACGATCTACCCGCGCATTTCAGCCACCAGGGCTGACTGAACTTTACCCAGTCCCGGCGCGGGAGGAGGA
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CCTTTTTTTCTGAACGATCTACCCGCGCATTTCAGCCACCAGGGCTGACTGAACTTTACCCAGTCCCGGCGCGGGAGGAGGA
          150       160       170       180       190       200       210

           220       230       240       250       260       270       280
   GAGGGCTGGGTCGTGTGACTTCAGTGCTGAGGTTGATCAAGGCAAGGGAGAAACTTCCTATTCCCAGACCCTTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GAGGGCTGGGTCGTGTGACTTCAGTGCTGAGGTTGATCAAGGCAAGGGAGAAACTTCCTATTCCCAGACCCTTT
          220       230       240       250       260       270       280

           290       300       310       320       330       340       350       360
   GCAAGAAAGAAATGGCATATTACTTGCCGCCGACAGGGGGTTATTATTACTAAAATGGAGTCAGTATAAAATGCTT
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GCAAGAAAGAAATGGCATATTACTTGCCGCCGACAGGGGGTTATTATTACTAAAATGGAGTCAGTATAAAATGCTT
          290       300       310       320       330       340       350       360
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

```
Sequence Name   Description              Init.   Opt.
                                         Score  Score  Sig. Frame
```